

H1CDR (26) GFNIKDSYMH (35)
H2CDR (50) WIDPENGDT EYAPKFQ (65)
H3CDR (99) GTPTGPYYFDY (109)
L1CDR (159) SASSSVSYMH (168)
L2CDR (184) STSNLAS (190)
L3CDR (223) QQRSSYPLT (231)

Fig. 1. Amino acid sequences of CAB1 CDRs

SEQ ID NO: 1

```
1  QVKLQQSGAE LVRSGTSVKL SCTASGFNIK DSYMHWLRQG PEQGLEWIGW
51 IDPENGDTHEY APKFOGKATF TTDTSSTAY LQLSSLTSED TAVYYCNEGT
101 PTGPYYFDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAISASP
151 GEKVTITCSA SSSVSYMHWF QQKPGTSPKL WIYSTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRSSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMKAQSV GMAVAVIYQG KPHYTTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
```

Fig. 2A Amino acid sequence of CAB1 protein

SEQ ID NO: 2

```
1 TPVSEKQLAE VVANTITPLM KAQSVPGMAV AVIYQGKPHY YTFGKADIAA
51 NKPVTPQTLF ELGSISKFTT GVLGGDAIAR GEISLDDAVT RYWPQLTGKQ
101 WQGIRMLDLA TYTAGGLPLQ VPDEVTDNAS LLRFYQNWQP QWKPGTTRLY
151 ANASIGLFGA LAVKPSGMPY EQAMTTRVLK PLKLDHTWIN VPKAEEAHYA
201 WGYRDGKAVR VSPGMLDAQA YGVKTNVQDM ANWVMANMAP ENVADASLKQ
251 GIALAQSRWY RIGSMYQGLG WEMLNWPVEA NTVVETSFGN VALAPLPVAE
301 VNPPAPPVKA SWVHKTGSTG GFGSYVAFIP EKQIGIVMLA NTSYPNPARV
351 EAAYHILEAL Q
```

Fig. 2B Amino acid sequence of BLA protein

SEQ ID NO: 3

H1CDR (26) GFNIKDSYMH (35)
H2CDR (50) WIDPENGDT EYAPKFQ (65)
H3CDR (99) GLPTGPYYFDY (109)
L1CDR (159) SASSSVSYMH (168)
L2CDR (184) DTSNLAS (190)
L3CDR (223) QQRDSYPLT (231)

Fig. 3A Amino acid sequences of CAB1.6 CDRs

H1CDR (26) GFNIKDSYMH (35)
H2CDR (50) WIDPENGDT EYAPKFQ (65)
H3CDR (99) GLPLGAIYNDY (109)
L1CDR (159) SASSAVYAMH (168)
L2CDR (184) DTSNLAS (190)
L3CDR (223) QQRDSYPLT (231)

Fig. 3B Amino acid sequences of CAB1.7 CDRs

```
1  QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51  IDPENGDTHEY APKFQGKATF TTDTSSTAY LQLSSLTSED TAVYYCNEGL
101 PTGPYYFDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMKAQSV GMAVAVIYQG KPHYITFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
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Fig. 4A Amino acid sequence of CAB1.6 protein

SEQ ID NO. 7

```
1  QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51  IDPENGDTY  APKFQ GKATF TTDTSNTAY LQLSSLTSED TAVYYCNEGL
101 PTGPYYFDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMAAQSPV GMAVAVIYQG KPHYITFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVET SFGNVALAPL PVAEVNPPAP
551 PVKASVHKT GSTGGFGAYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
```

Fig. 4B Amino acid sequence of CAB1.6i protein

SEQ ID NO: 8

```
1  QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51  IDPENGDT EY APKFQGKATF TTD TSSNTAY LQLSSLTSED TAVYYCNEGL
101 PLGAIYNDYW GQGTTVT VSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSAVYAMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMKAQSV GMAVAVIYQG KPHY YTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEV T DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
```

Fig. 5A Amino acid sequence of CAB1.7 protein

SEQ ID NO: 9


```
1  QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51  IDPENGDTY APKFQ GKATF TTDTSSNTAY LQLSSLTSED TAVYYCNEGL
101 PLGAIYNDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSAVYAMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMAAQSV GMAVAVIYQG KPHYITFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEV DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASVHKT GSTGGFGAYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
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Fig. 5B Amino acid sequence of CAB1.7i protein

SEQ ID NO: 10

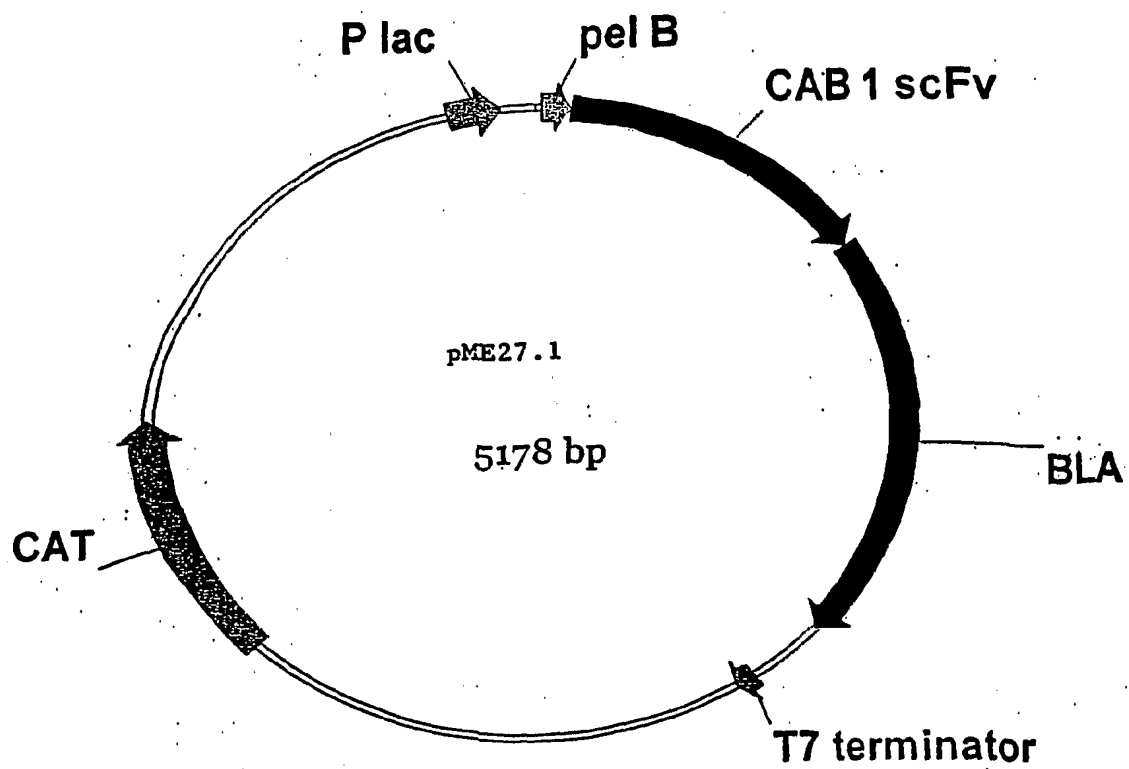


Figure 6A

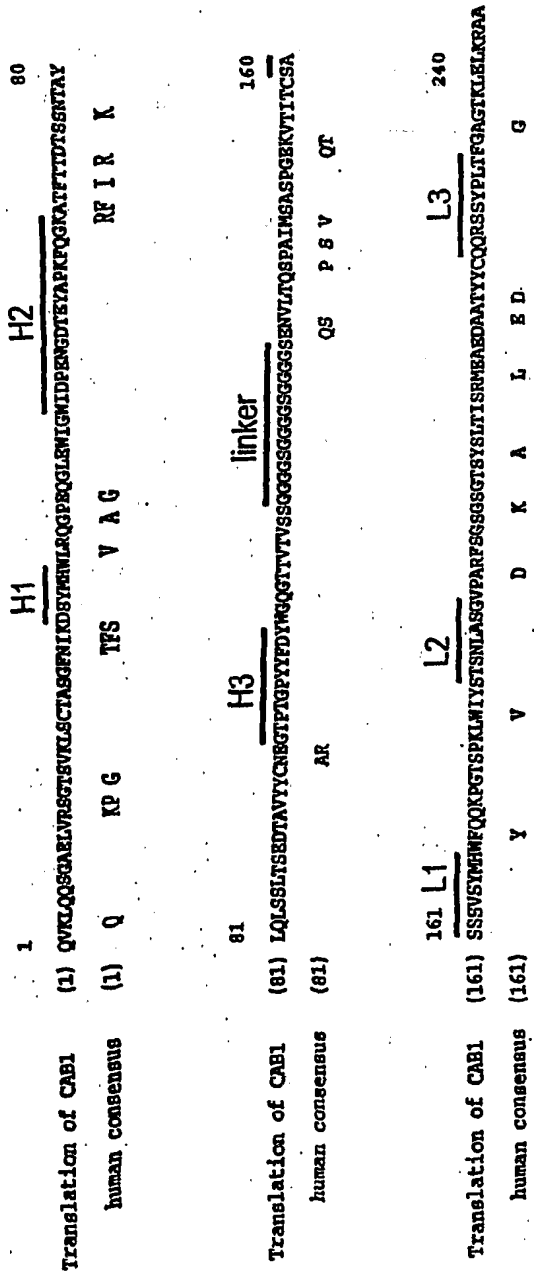


Figure 6B

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Figure 6C —

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heavy chain:
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linker:
 gggsgggsgggsgggsg

light chain:
 envltqspaimsaspgkevlticsasssvsymhwhfqkpgtspkklwystsnlasgvparfsgsgtsysltismcaedaatyccqrrssypiltfgagtklelkraat

BLA:
 pvsekqlaevvantitplmkaqsvpgmnaviyqgkphyytfgkadiaankpvtptlflgskstftglggdaiaargeislddavtrywppqltgkqwqgirmldlatytagglpqpdevtd
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Figure 6D

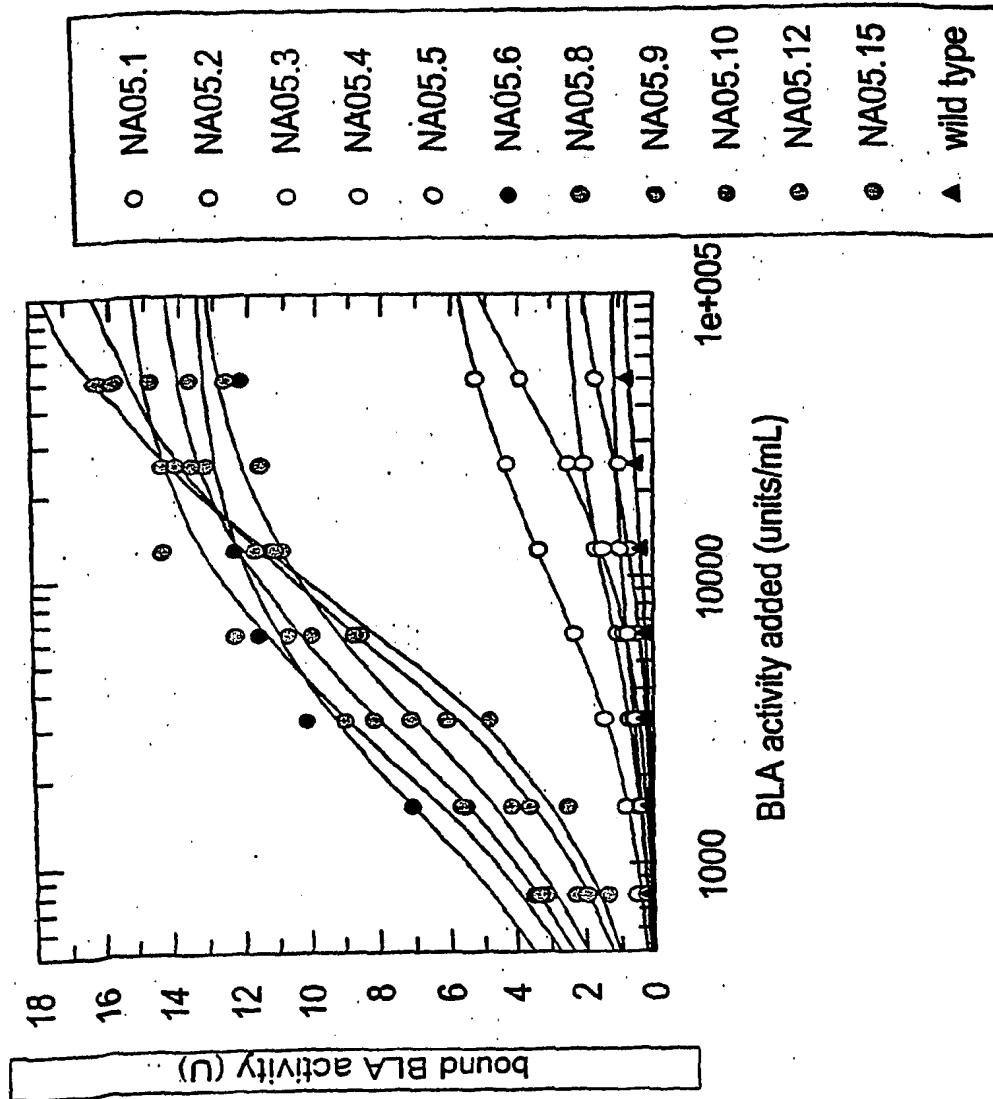


Figure7A

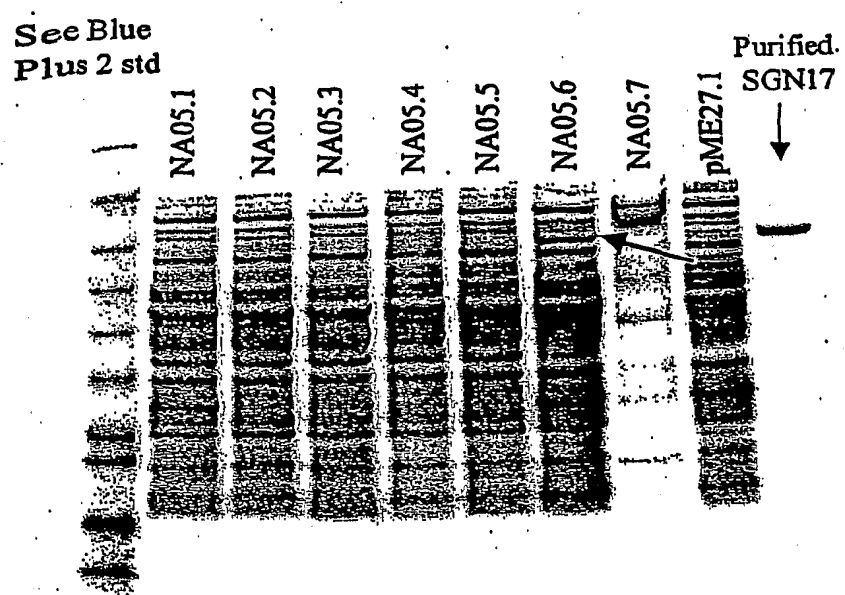


Figure 7B

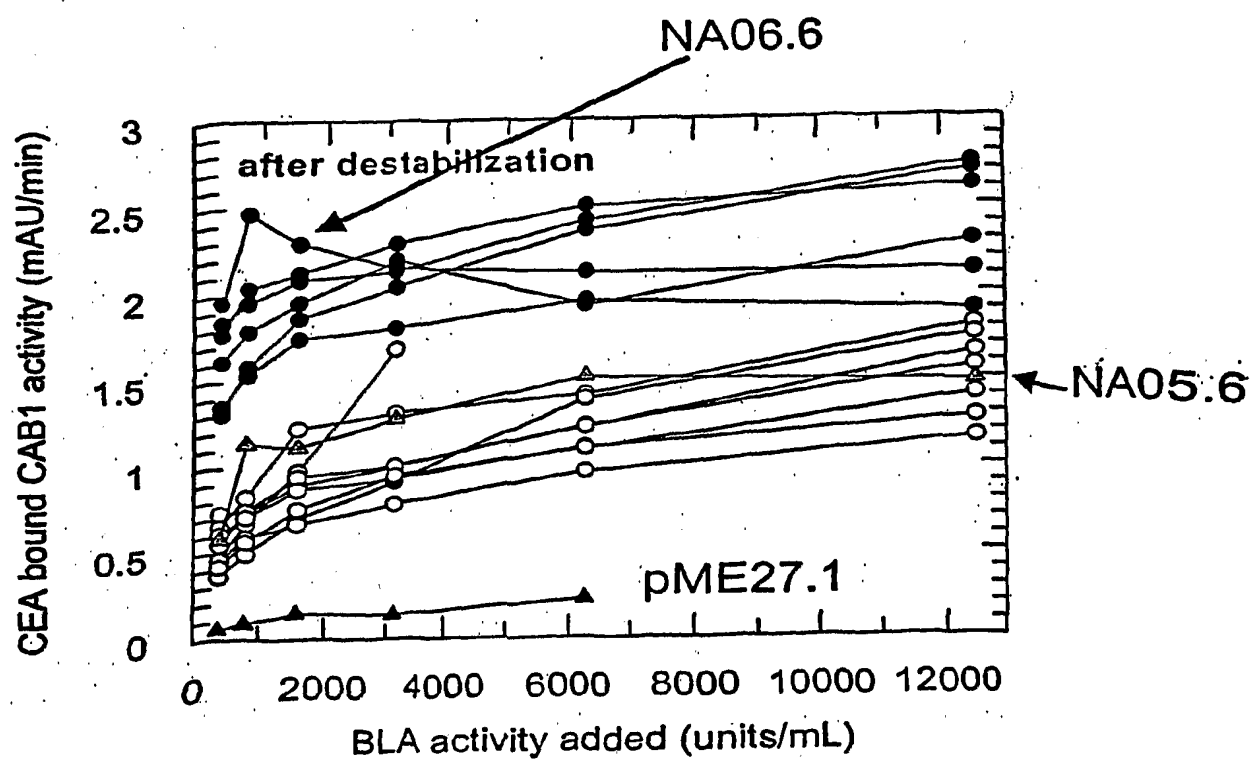


Figure 7C

pos. heavy chain	number of observations	observed frequencies of 5 most abundant amino acids in alignment of human sequences												CAB1 sequence	CDR	mutated residues
1	291	E	0.616	Q	0.346	D	0.014	G	0.014	A	0.003	L	0.003	Q		
2	293	V	0.887	M	0.027	L	0.024	S	0.020	I	0.017	A	0.007	V		
3	291	Q	0.852	H	0.034	R	0.027	T	0.027	E	0.014	V	0.014	K		1
4	282	L	0.975	V	0.011	A	0.007	D	0.004	M	0.004			L		
5	276	V	0.645	Q	0.148	L	0.120	R	0.022	M	0.014	N	0.014	Q		
6	267	E	0.693	Q	0.263	A	0.022	D	0.011	G	0.007	R	0.004	Q		
7	265	S	0.951	W	0.019	X	0.015	T	0.008	A	0.004	N	0.004	S		
8	266	G	0.989	S	0.008	T	0.004							G		
9	274	G	0.624	A	0.193	P	0.164	S	0.011	E	0.004	H	0.004	A		
10	271	G	0.638	E	0.192	D	0.081	A	0.070	T	0.011	V	0.007	E		
11	270	L	0.681	V	0.270	F	0.030	S	0.019					L		
12	267	V	0.757	K	0.154	I	0.026	N	0.022	L	0.015	A	0.007	V		
13	247	K	0.474	Q	0.428	R	0.049	E	0.034	G	0.004	H	0.004	R		1
14	251	P	0.968	A	0.012	K	0.008	G	0.004	L	0.004	S	0.004	S		1
15	244	G	0.783	S	0.156	T	0.033	P	0.016	K	0.008	E	0.004	G		
16	243	G	0.488	E	0.131	Q	0.107	A	0.094	R	0.082	S	0.066	T		1
17	234	S	0.766	T	0.204	A	0.009	F	0.009	P	0.004	R	0.004	S		
18	244	L	0.812	V	0.155	M	0.008	A	0.004	E	0.004	F	0.004	V		
19	242	R	0.545	K	0.240	S	0.161	T	0.037	A	0.012	Q	0.004	K		
20	246	L	0.736	V	0.191	I	0.061	E	0.004	R	0.004	X	0.004	L		
21	218	S	0.729	T	0.234	G	0.009	I	0.009	A	0.005	D	0.005	S		
22	217	C	0.991	R	0.005	S	0.005							C		
23	231	A	0.558	K	0.203	T	0.117	E	0.048	V	0.022	I	0.013	T		
24	235	A	0.638	V	0.174	G	0.064	I	0.055	T	0.030	F	0.026	A		
25	226	S	0.951	Y	0.027	F	0.009	C	0.004	K	0.004	T	0.004	S		
26	225	G	0.956	E	0.013	A	0.009	D	0.009	S	0.009	V	0.004	G		
27	213	F	0.559	Y	0.164	G	0.150	D	0.080	S	0.019	L	0.014	F		
28	203	T	0.571	S	0.286	I	0.049	N	0.049	P	0.015	A	0.005	N		1
29	207	F	0.749	V	0.111	I	0.068	L	0.053	T	0.010	A	0.005	I		1
30	202	S	0.762	T	0.119	N	0.035	G	0.020	R	0.020	A	0.010	K		1
31	199	S	0.482	T	0.136	D	0.104	N	0.087	G	0.060	K	0.040	D	H1	
32	202	Y	0.535	S	0.144	N	0.083	A	0.069	D	0.031	G	0.030	S	H1	
33	197	A	0.269	Y	0.162	G	0.147	W	0.117	S	0.091	T	0.066	Y	H1	
34	200	M	0.520	I	0.210	W	0.070	A	0.055	Y	0.050	V	0.040	M	H1	
35	196	S	0.372	H	0.235	N	0.077	A	0.061	G	0.051	Y	0.046	H	H1	
35a	33	-	0.824	W	0.096	V	0.043	G	0.016	S	0.016	N	0.005		H2	
35b	27	-	0.856	N	0.064	G	0.037	S	0.032	A	0.005	R	0.005		H3	
36	192	W	0.990	M	0.005	T	0.005							W		
37	193	V	0.741	I	0.228	L	0.021	G	0.005	Q	0.005			L		1
38	190	R	0.989	P	0.005	V	0.005							R		
39	190	Q	0.979	T	0.011	G	0.005	R	0.005					Q		
40	191	A	0.634	P	0.199	S	0.073	M	0.052	G	0.010	V	0.010	G		1
41	187	P	0.914	S	0.043	T	0.021	A	0.005	L	0.005	Q	0.005	P		
42	187	G	0.925	S	0.064	P	0.005	R	0.005					E		1
43	186	K	0.683	Q	0.183	R	0.124	E	0.005	H	0.005			Q		
44	186	G	0.882	A	0.048	S	0.043	R	0.027					G		
45	186	L	0.978	P	0.022									L		
46	185	E	0.956	Q	0.039	V	0.005							E		
47	184	W	0.989	S	0.011									W		

Figure 8A —

48	185	V	0.481	M	0.216	I	0.173	L	0.124			I			
49	185	G	0.600	S	0.216	A	0.162	E	0.005	L	0.005	G			
50	185	R	0.146	W	0.146	V	0.119	A	0.114	G	0.081	Y	0.081	W	H2
51	185	I	0.822	T	0.081	R	0.027	V	0.022	K	0.016	M	0.011	I	H2
52	184	S	0.250	Y	0.239	N	0.123	K	0.060	I	0.054	D	0.050	D	H2
52a	141	-	0.230	P	0.180	Y	0.153	G	0.126	N	0.066	V	0.055	P	H2
52b	34	-	0.814	K	0.115	R	0.060	G	0.005	Y	0.005				H2
52c	22	-	0.880	T	0.044	V	0.033	S	0.022	A	0.011	G	0.005		H2
53	184	S	0.228	D	0.163	Y	0.125	G	0.109	N	0.082	H	0.054	E	H2
54	183	G	0.328	S	0.202	D	0.129	N	0.112	K	0.082	F	0.055	N	H2
55	182	G	0.544	S	0.181	D	0.085	W	0.066	Y	0.060	N	0.020	G	H2
56	182	S	0.231	D	0.182	N	0.147	T	0.143	Y	0.077	G	0.060	D	H2
57	184	T	0.582	K	0.120	N	0.065	A	0.054	I	0.054	P	0.022	T	H2
58	183	Y	0.322	N	0.216	D	0.139	R	0.060	H	0.055	T	0.038	E	H2
59	184	Y	0.908	F	0.043	N	0.016	S	0.011	D	0.005	G	0.005	Y	H2
60	183	A	0.579	N	0.153	S	0.104	T	0.055	R	0.044	G	0.027	A	H2
61	184	D	0.277	P	0.239	Q	0.174	A	0.141	V	0.076	T	0.033	P	H2
62	185	S	0.686	K	0.146	P	0.065	N	0.038	G	0.016	R	0.016	K	H2
63	186	V	0.511	L	0.247	F	0.215	S	0.011	A	0.005	K	0.005	F	H2
64	186	K	0.581	Q	0.274	R	0.054	N	0.032	E	0.022	T	0.022	Q	H2
65	186	G	0.688	S	0.237	T	0.032	A	0.016	D	0.011	E	0.011	G	H2
66	186	R	0.935	Q	0.054	H	0.005	I	0.005					K	1
67	186	F	0.462	V	0.409	I	0.065	L	0.054	A	0.005	S	0.005	A	1
68	186	T	0.914	I	0.038	A	0.016	S	0.011	K	0.005	N	0.005	T	
69	187	I	0.791	M	0.139	V	0.032	D	0.005	F	0.005	G	0.005	F	1
70	187	S	0.684	T	0.214	N	0.070	L	0.032					T	
71	187	R	0.529	V	0.160	A	0.107	P	0.064	T	0.053	K	0.043	T	1
72	186	D	0.902	N	0.071	K	0.016	E	0.011					D	
73	185	T	0.368	N	0.266	D	0.177	K	0.070	E	0.059	A	0.011	T	
74	186	S	0.946	A	0.048	L	0.005							S	
75	187	K	0.674	T	0.139	I	0.070	R	0.027	A	0.021	F	0.021	S	1
76	187	N	0.701	S	0.251	K	0.027	R	0.011	T	0.005	Y	0.005	N	
77	187	T	0.615	Q	0.273	S	0.048	M	0.021	L	0.016	P	0.011	T	
78	186	L	0.364	A	0.273	F	0.235	V	0.096	I	0.005	M	0.005	A	
79	187	Y	0.638	S	0.239	F	0.059	V	0.048	H	0.005	M	0.005	Y	
80	187	L	0.782	M	0.207	N	0.005	-	0.005					L	
81	187	Q	0.529	E	0.205	K	0.122	R	0.032	T	0.032	N	0.027	Q	
82	194	M	0.497	L	0.421	W	0.051	V	0.015	I	0.010	-	0.005	L	
82a	195	N	0.442	S	0.291	R	0.077	T	0.066	D	0.053	G	0.020	S	
82b	194	S	0.795	N	0.082	R	0.051	G	0.026	T	0.021	A	0.010	S	
82c	197	L	0.701	V	0.234	M	0.041	G	0.010	A	0.005	D	0.005	L	
83	197	R	0.528	T	0.239	K	0.122	D	0.041	E	0.020	Q	0.015	T	
84	198	A	0.495	P	0.182	S	0.177	T	0.051	I	0.035	V	0.030	S	
85	198	E	0.591	A	0.172	D	0.126	S	0.051	V	0.045	G	0.015	E	
86	198	D	0.975	T	0.010	V	0.010	N	0.005					D	
87	198	T	0.929	S	0.035	G	0.010	M	0.010	A	0.005	Q	0.005	T	
88	198	A	0.939	G	0.040	P	0.005	T	0.005	V	0.005	Y	0.005	A	
89	198	V	0.768	L	0.066	M	0.056	T	0.045	I	0.040	F	0.010	V	
90	199	Y	0.980	F	0.010	A	0.005	I	0.005					Y	
91	199	Y	0.930	F	0.045	C	0.015	R	0.005	T	0.005			Y	
92	198	C	0.990	A	0.005	M	0.005							C	
93	198	A	0.838	T	0.076	V	0.061	H	0.005	K	0.005	N	0.005	N	1
94	198	R	0.596	K	0.162	T	0.051	G	0.045	P	0.045	Q	0.025	E	1
95	161	G	0.174	D	0.120	E	0.099	A	0.093	N	0.092	P	0.068	G	
96	159	P	0.168	R	0.130	G	0.112	L	0.062	V	0.062	Y	0.062	T	H3
97	156	G	0.170	P	0.094	V	0.094	E	0.088	T	0.069	S	0.063	P	H3
98	155	G	0.152	Y	0.101	L	0.095	D	0.087	V	0.076	S	0.063	T	H3

pos. light chain	number of observations	observed frequencies of 5 most abundant amino acids in alignment of human sequences												CAB1 sequence	CDR	mutated residues
		Q	S	N	H	D	F	E	T	L	V	A	I			
1	95	Q	0.589	S	0.158	N	0.095	H	0.074	D	0.053	F	0.021	E		1
2	139	S	0.446	Y	0.388	F	0.101	V	0.043	L	0.014	T	0.007	N		1
3	140	V	0.307	E	0.243	A	0.207	M	0.093	D	0.064	I	0.043	V		
4	140	L	0.971	V	0.029									L		
5	141	T	0.915	A	0.021	S	0.021	I	0.014	K	0.007	L	0.007	T		
6	140	Q	0.993	E	0.007									Q		
7	139	P	0.906	D	0.029	S	0.029	A	0.022	E	0.014			S		1
8	139	P	0.741	A	0.137	H	0.072	R	0.029	L	0.007	S	0.007	P		
9	139	S	0.964	A	0.014	V	0.014	R	0.007					A		1
10	0	-	1.000											I		1
11	138	V	0.790	A	0.138	L	0.058	M	0.014					M		1
12	139	S	0.978	F	0.007	T	0.007	E	0.004	Q	0.004			S		
13	138	V	0.406	G	0.348	A	0.138	E	0.087	L	0.014	D	0.007	A		
14	135	S	0.630	A	0.230	T	0.111	D	0.007	F	0.007	G	0.007	S		
15	135	P	0.881	L	0.089	A	0.022	S	0.007					P		
16	134	G	0.978	E	0.015	L	0.007							G		
17	133	Q	0.811	K	0.098	A	0.045	E	0.024	G	0.015	H	0.008	E		1
18	133	T	0.504	S	0.263	R	0.135	K	0.068	E	0.008	G	0.008	K		1
19	130	V	0.454	A	0.385	I	0.146	G	0.008	L	0.008			V		
20	128	T	0.531	R	0.188	S	0.148	K	0.047	I	0.031	M	0.016	T		
21	121	I	0.901	V	0.050	L	0.017	A	0.008	F	0.008	M	0.008	I		
22	120	S	0.492	T	0.475	A	0.008	G	0.008	I	0.008	N	0.008	T		
23	117	C	1.000											C		
24	112	S	0.536	T	0.259	G	0.089	A	0.045	Q	0.033	I	0.018	S	L1	
25	108	G	0.870	L	0.056	R	0.028	A	0.019	I	0.009	P	0.009	A	L1	
26	108	D	0.339	S	0.250	T	0.213	N	0.087	E	0.037	G	0.037	S	L1	
27	104	S	0.415	N	0.118	K	0.113	A	0.104	T	0.066	G	0.047	S	L1	
28	104	L	0.346	S	0.346	I	0.115	G	0.067	A	0.058	D	0.019	S	L1	
29	100	G	0.243	N	0.239	D	0.159	S	0.078	P	0.068	H	0.058	V	L1	
30	103	I	0.291	V	0.165	D	0.136	N	0.107	E	0.058	S	0.049	S	L1	
31	101	G	0.356	K	0.168	A	0.099	E	0.084	Q	0.084	D	0.069	Y	L1	
31a	54	-	0.438	S	0.167	G	0.104	N	0.083	Y	0.063	D	0.052	M	L1	
31b	49	-	0.495	N	0.227	Y	0.155	S	0.041	G	0.021	H	0.021	H	L1	
31c	23	-	0.760	N	0.134	S	0.031	K	0.021	D	0.012	E	0.010		L1	
31d	0	-	1.000												L1	
31e	0	-	1.000												L1	
31f	0	-	1.000												L1	
32	94	Y	0.515	S	0.134	F	0.093	A	0.072	T	0.052	H	0.041		L1	
33	97	V	0.680	A	0.186	I	0.082	Y	0.021	F	0.010	P	0.010		L1	
34	92	S	0.380	H	0.120	A	0.109	Y	0.098	N	0.076	Q	0.076		L1	
35	98	W	0.990	Y	0.010									W		
36	96	Y	0.844	F	0.073	H	0.073	W	0.010					F		1
37	95	Q	0.916	R	0.042	E	0.011	H	0.011	K	0.011	Y	0.011	Q		
38	94	Q	0.862	H	0.053	L	0.053	E	0.011	K	0.011	V	0.011	Q		
39	93	K	0.333	L	0.172	R	0.161	H	0.151	Q	0.086	V	0.043	K		
40	93	P	0.946	S	0.022	A	0.011	L	0.011	R	0.011			P		

Figure 8B -

41	93	G	0.871	H	D	0.022	R	0.022	P	0.011	G	0.011	G		
42	92	Q	0.424	T	0.217	K	0.163	R	0.087	S	0.011	G	0.022	T	
43	92	A	0.717	S	0.174	G	0.065	T	0.022	L	0.011	V	0.011	S	
44	93	P	0.978	A	0.011	M	0.011							P	
45	92	K	0.391	V	0.315	R	0.109	L	0.065	T	0.065	A	0.033	K	
46	92	L	0.728	V	0.076	F	0.065	T	0.043	A	0.022	M	0.022	L	
47	91	V	0.484	L	0.374	I	0.077	M	0.055	N	0.011			W	1
48	91	I	0.791	V	0.110	M	0.077	L	0.011	S	0.011			I	
49	91	Y	0.769	F	0.110	R	0.066	H	0.022	D	0.011	I	0.011	Y	
50	89	D	0.303	E	0.210	Q	0.093	V	0.067	G	0.056	K	0.056	S	L2
51	88	D	0.364	N	0.205	V	0.159	H	0.068	T	0.068	G	0.034	T	L2
52	89	N	0.393	T	0.213	S	0.202	D	0.101	A	0.022	F	0.011	S	L2
53	88	K	0.307	D	0.193	Q	0.182	N	0.080	E	0.057	S	0.057	N	L2
54	88	R	0.875	X	0.068	K	0.034	L	0.011	W	0.011			L	L2
55	86	P	0.851	G	0.080	S	0.023	A	0.011	H	0.011	R	0.011	A	L2
56	85	S	0.837	D	0.081	P	0.023	A	0.012	L	0.012	T	0.012	S	L2
57	86	G	0.920	E	0.034	S	0.011	T	0.011	W	0.011	-	0.011	G	
58	84	I	0.600	V	0.353	A	0.012	G	0.012	T	0.012	-	0.012	V	
59	84	P	0.847	S	0.106	A	0.012	L	0.012	V	0.012	-	0.012	P	
60	85	D	0.488	E	0.325	N	0.047	A	0.035	H	0.023	L	0.023	A	1
61	87	R	0.977	D	0.011	-	0.011							R	
62	88	F	0.943	I	0.034	L	0.011	R	0.011					F	
63	87	S	0.989	F	0.011									S	
64	87	G	0.885	A	0.069	S	0.023	V	0.023					G	
65	87	S	0.977	G	0.011	Y	0.011							S	
66	86	K	0.430	N	0.186	S	0.186	T	0.081	X	0.070	R	0.035	G	1
67	85	S	0.953	T	0.024	K	0.012	L	0.012					S	
68	85	G	0.859	S	0.071	A	0.035	D	0.024	Q	0.012			G	
69	85	N	0.434	T	0.318	A	0.129	D	0.036	G	0.024	K	0.024	T	
70	85	T	0.529	S	0.341	E	0.082	A	0.024	K	0.024			S	
71	85	A	0.847	R	0.082	V	0.059	S	0.012					Y	1
72	85	T	0.447	S	0.424	Y	0.082	A	0.035	I	0.012			S	
73	85	L	0.988	S	0.012									L	
74	85	T	0.706	A	0.165	G	0.106	I	0.012	L	0.012			T	
75	85	I	0.929	V	0.047	A	0.012	L	0.012					I	
76	85	S	0.718	T	0.200	N	0.035	I	0.024	G	0.012	R	0.012	S	
77	85	G	0.765	R	0.129	S	0.094	E	0.012					R	
78	85	L	0.588	V	0.224	T	0.106	A	0.071	G	0.012			M	1
79	85	Q	0.659	E	0.153	R	0.071	K	0.047	L	0.024	A	0.012	E	
80	85	A	0.459	S	0.235	T	0.200	V	0.047	P	0.035	N	0.012	A	
81	85	E	0.541	G	0.235	M	0.071	D	0.047	L	0.024	N	0.024	E	
82	85	D	0.964	N	0.024	E	0.012							D	
83	85	E	0.976	D	0.012	T	0.012							A	1
84	85	A	0.941	T	0.035	E	0.012	S	0.012					A	
85	85	D	0.859	E	0.082	H	0.024	A	0.012	I	0.012	M	0.012	T	1
86	85	Y	0.976	F	0.012	H	0.012							Y	
87	85	Y	0.894	F	0.106									Y	
88	85	C	0.988	H	0.012									C	
89	85	Q	0.482	A	0.153	S	0.141	G	0.094	C	0.059	N	0.035	Q	L3
90	85	S	0.388	T	0.271	A	0.212	V	0.118	L	0.012			Q	L3
91	85	W	0.576	Y	0.247	A	0.059	F	0.035	R	0.035	D	0.012	R	L3
92	84	D	0.606	G	0.095	A	0.071	N	0.061	T	0.048	E	0.024	S	L3
93	84	S	0.405	D	0.179	G	0.107	N	0.095	P	0.071	T	0.060	S	L3
94	84	S	0.536	G	0.155	N	0.073	R	0.060	D	0.058	T	0.048	Y	L3
95	82	S	0.265	L	0.253	G	0.108	N	0.096	T	0.084	A	0.036	P	L3

Figure 8B - 2

95a	60	-	0.268	S	0.183	D	0.159	N	0.110	T	0.073	Q	0.049	L	L3	
95b	40	-	0.512	A	0.098	G	0.098	H	0.085	E	0.049	R	0.037	T	L3	
95c	5	-	0.939	P	0.037	A	0.012	G	0.012						L3	
95d	1	-	0.988	G	0.012										L3	
95e	0	-	1.000												L3	
95f	0	-	1.000												L3	
96	80	V	0.305	G	0.098	P	0.098	W	0.098	A	0.073	N	0.073		L3	
97	85	V	0.788	I	0.118	L	0.047	M	0.035	G	0.012			F		
98	86	F	0.988	V	0.012									G		
99	89	G	0.989	F	0.011									A		1
100	89	G	0.831	T	0.124	A	0.022	S	0.022					G		
101	89	G	1.000											T		
102	89	T	0.989	G	0.011									K		
103	88	K	0.739	N	0.091	R	0.068	Q	0.034	T	0.034	E	0.011	L		
104	87	L	0.667	V	0.322	Q	0.011							E		1
105	87	T	0.954	S	0.023	I	0.011	L	0.011					L		1
106	85	V	0.988	T	0.012									K		1
106a	84	L	0.952	V	0.024	P	0.012	Q	0.012					R		1
107	78	G	0.782	S	0.103	R	0.090	C	0.013	L	0.013			A		1
108	46	Q	0.957	P	0.022	R	0.022							A		1
109	46	P	0.957	K	0.022	Q	0.022									

Figure 8B - 3

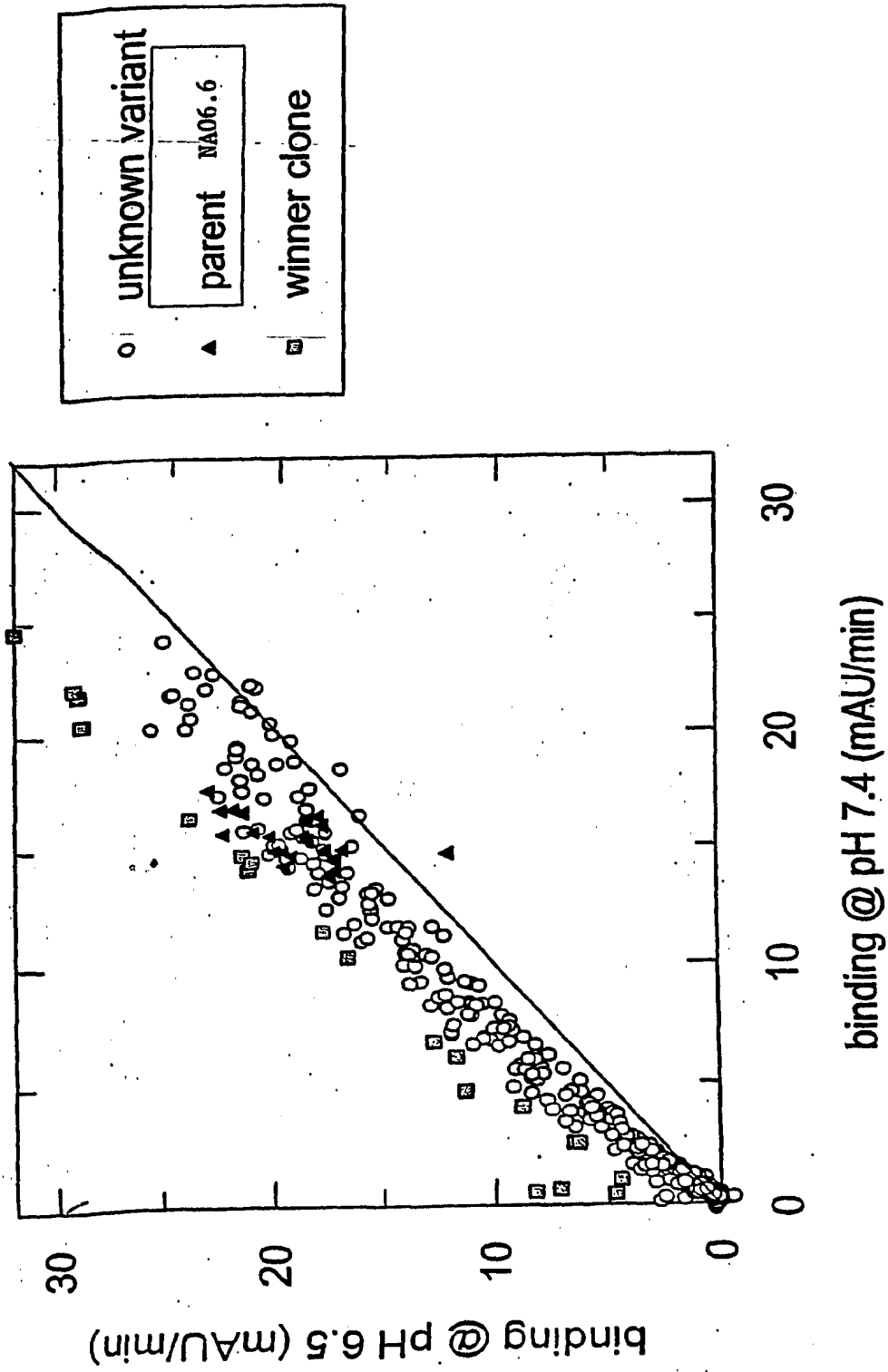


Figure 9

Residues chosen for
mutagenesis in NA06.6

CDRs in NA06.6

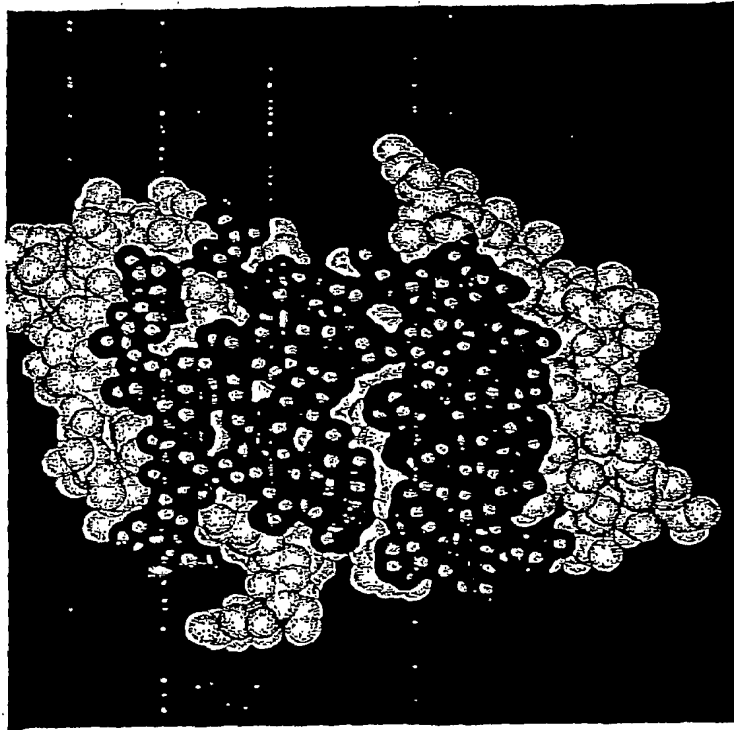
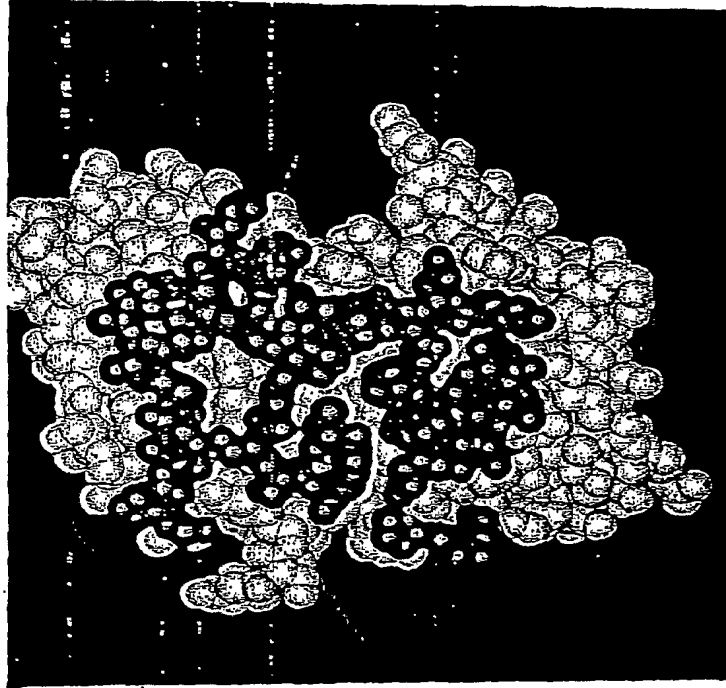


Figure 10

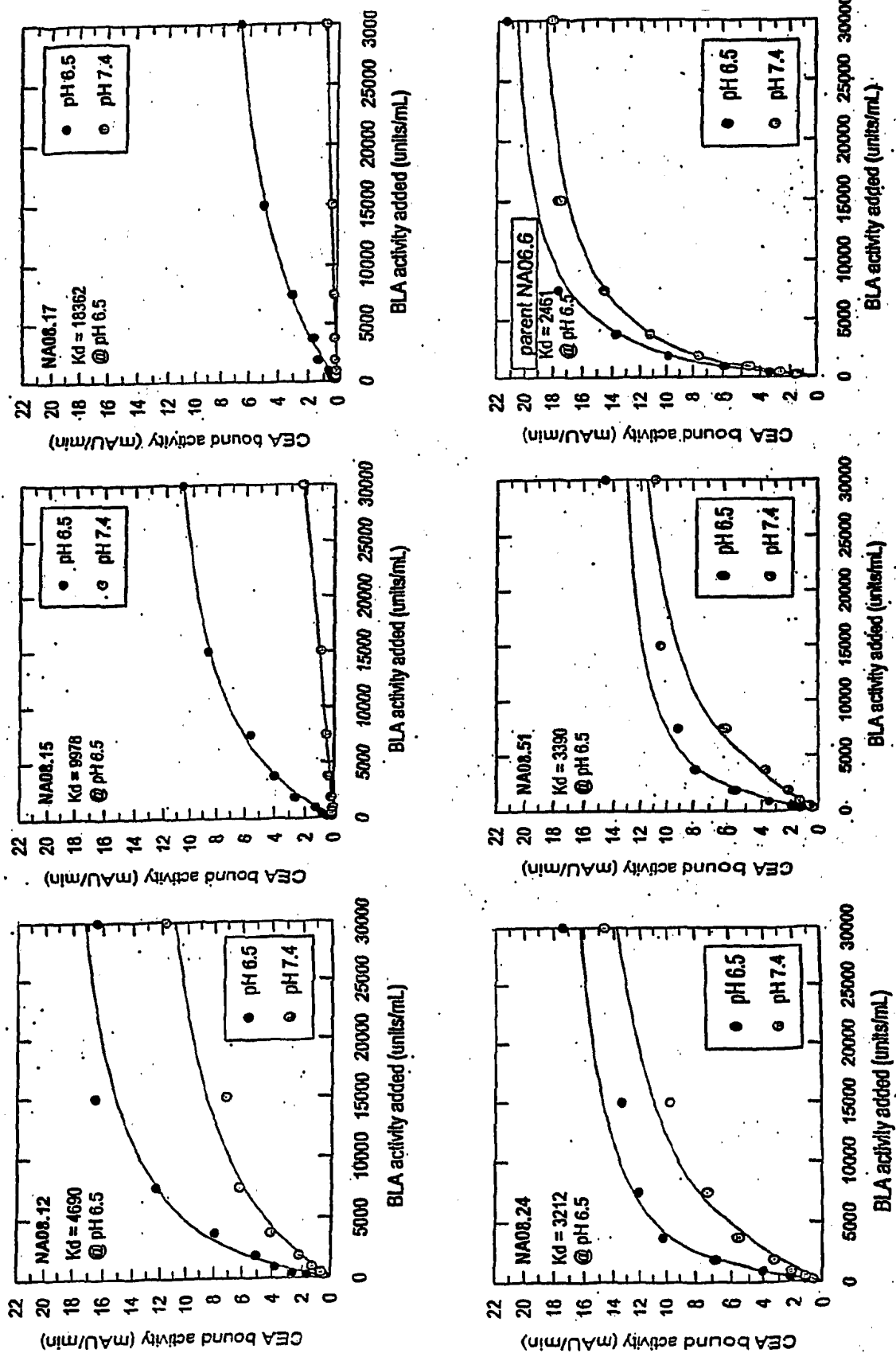


Figure 11

Figure 12: CAB1 engineering - summary

protein	changes	comments
CAB1	parent	
CAB1.1(NA05.6)	R13K, T16G, W181V	increase stability
CAB1.2(NA06.6)	K3Q, L37V, M146V	increase stability
CAB1.4(NA08.15)	S184D, S226D	pH-dependent binding
CAB1.6	T100L	increased affinity
SW149.5	T102L, P104A, Y105I, F107N	increased affinity
CAB1.7	S163T, S165Y, Y166S	increased affinity
CAB1.7i	in BLA: K265A, S568A	remove T-cell epitopes


cumulative changes


Figure 13: Binding of various CAB1 variants to immobilized CEA

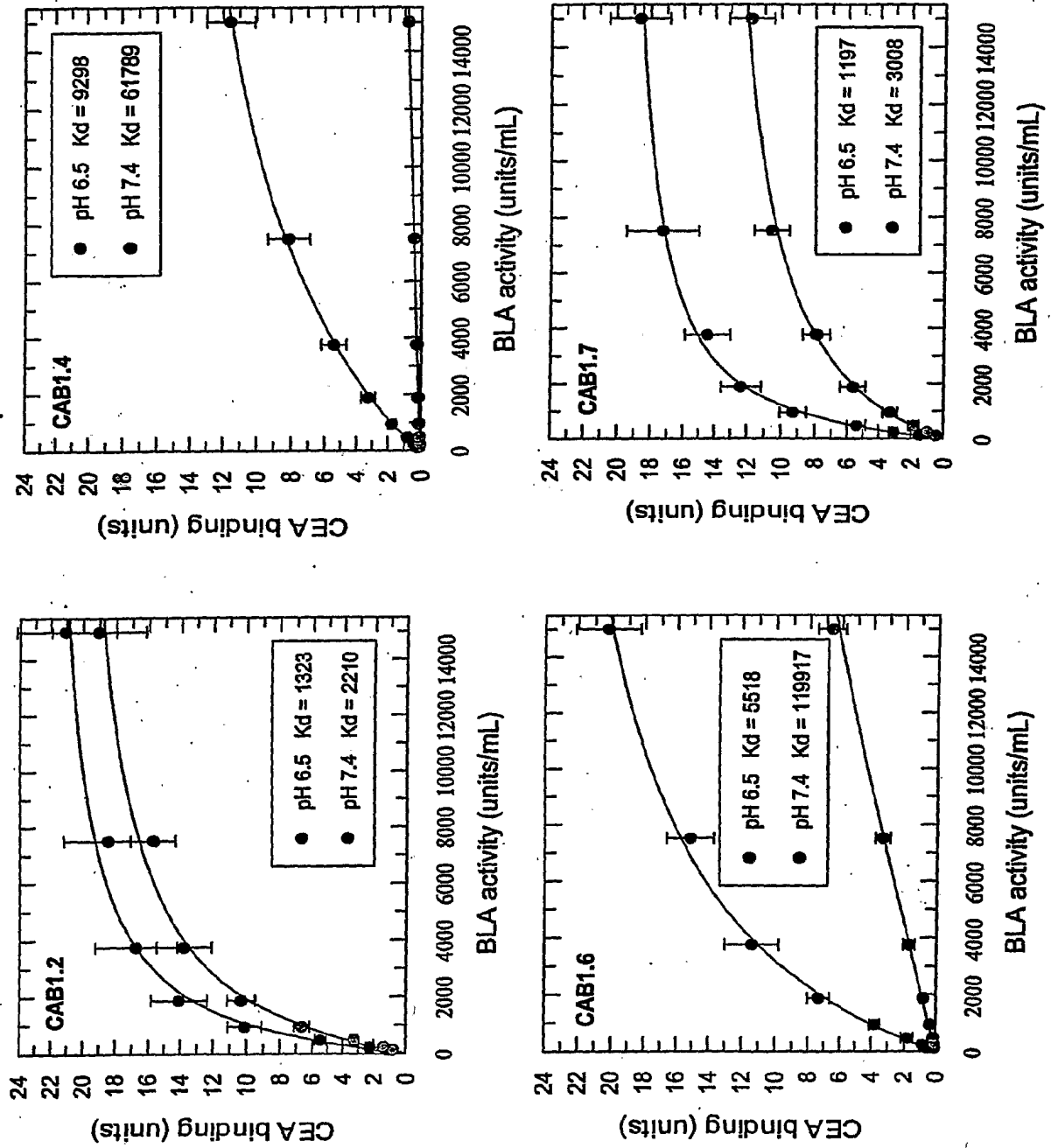
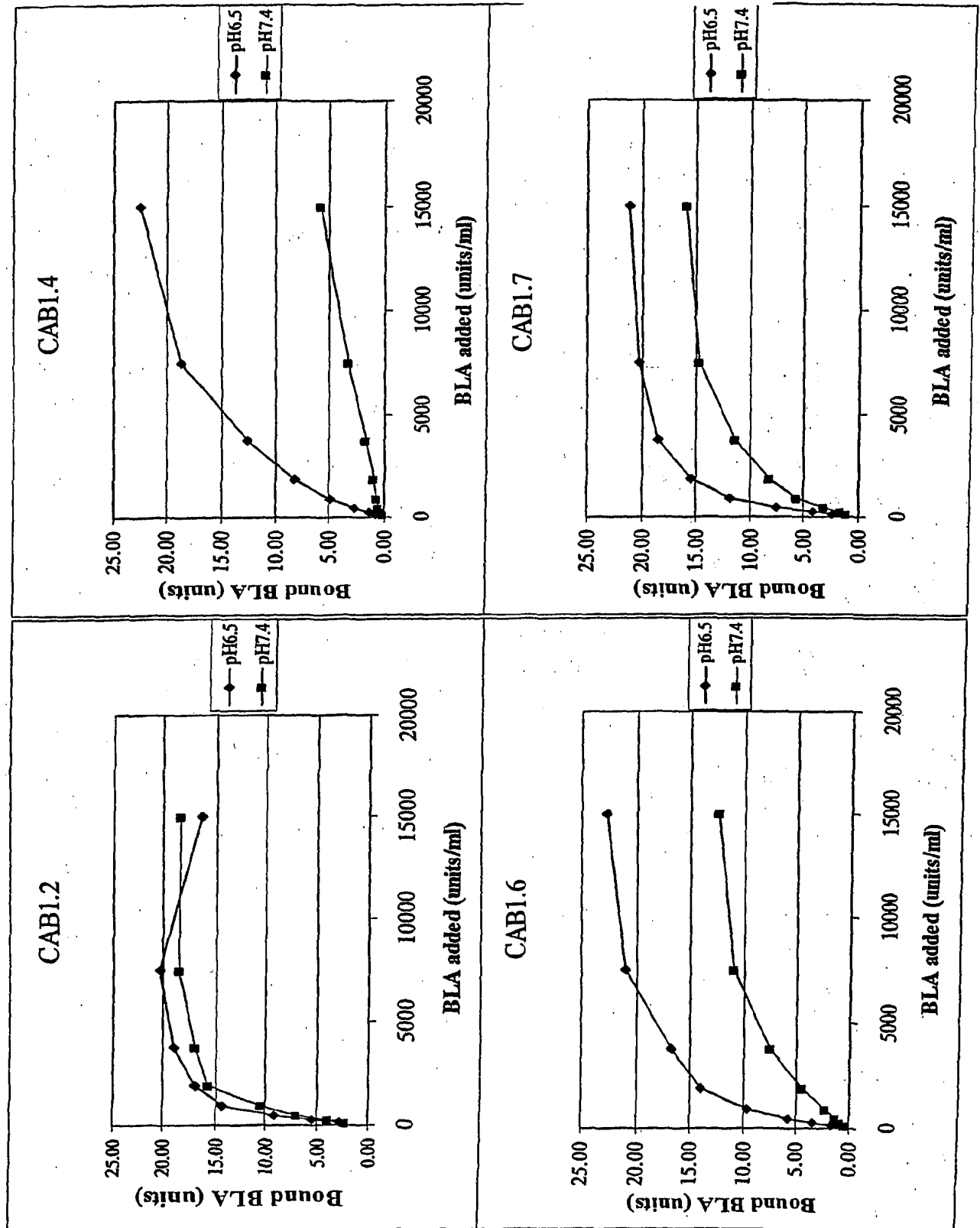


Figure 14: Binding of various CAB1 variants to LS174T cells

1	QVQLQQSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
51	IDPENGDT	APKFQGKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGL
101	PLGAIYNDYW	GQGTTVTVSS	GGGGSGGGGS	GGGGSENVLT	QSPAIVSASP
151	GEKVTITCSA	SSSVSYMHWF	QQKPGTSPKL	VIYDTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQQRDSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI	TPLMKAQSVP	GMAVAVIYQG	KPHYYTEFGKA	DIAANKPVTP
301	QTLFELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT	DNASLLRFYQ	NWQPQWKPGT	TRLYANASIG
401	LFGALAVKPS	GMPYEQAMTT	RVLKPLKLDH	TWINVPKAE	AHYAWGYRDG
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKOGIALAQ
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	PVAEVNPPAP
551	PVKASWVHKT	GSTGGFGSYV	AFTPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ				

Fig. 15A Amino acid sequence of SW149.5 protein

```
1  QVKLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWLRQG PEQGLEWIGW
51 IDPENGDTY APKFQ GKATF TTDTSNTAY LQLSSLTSED TAVYYCNEGT
101 PTGPYYFDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAISASP
151 GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYSTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRSSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMKAQSVP GMAVAVIYQG KPHYTTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQFQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
```

Fig. 15B Amino acid sequence of CAB1.1 protein

```

1  CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCAGTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGACT
301 CCGACTGGGC CGTACTACTT TGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAACCTC GTGATTTATA
551 GCACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGATCTAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCATATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

```

Fig. 15C Nucleotide sequence of CAB1.2 gene

1	QVQLOQSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
51	IDPENGDEY	APKFQ GKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEG
101	PTGPYYFDYW	GQGTTVTVSS	GGGSGGGGS	GGGSENVLT	QSPAIVSASP
151	GEKVTITCSA	SSSVSYMHWF	QKPGTSPKL	VIYSTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQQRSSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI	TPLMKAQSV	GMAVAVIYQG	KPHYYTFGKA	DIAANKPVTP
301	QTLFELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT	DNASLLRFYQ	NWQPQWKPGT	TRLYANASIG
401	LFGALAVKPS	GMPYEQAMTT	RVLKPLKLDH	TWINVPKAE	AHYAWGYRDG
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKQGIALAQ
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	PVAEVNPPAP
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ				

Fig. 15D Amino acid sequence of CAB1.2 protein

H1CDR (26) GFNIKDSYMH (35)
H2CDR (50) WIDPENGDT EYAPKFQ (65)
H3CDR (99) GTPTGPYYFDY (109)
L1CDR (159) SASSSVSYMH (168)
L2CDR (184) DTSNLAS (190)
L3CDR (223) QQRDSYPLT (231)

Fig. 15E Amino acid sequences of CAB1.4 CDRs

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC (183)
H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)
H3CDR (373) GGGACTCCGACTGGGCCGTACTACTTTGACTAC (405)
L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC (582)
L2CDR (628) GATACATCCAACCTGGCTTCT (648)
L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG (771)

Fig. 15F Nucleotide sequence of CAB1.4 CDRs

```

1  CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51  AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCAC TGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGACT
301 CCGACTGGGC CGTACTACTT TGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAACCTC GTGATTTATG
551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGA GCGCTGGACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCA TGGA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

```

Fig. 15G. Nucleotide sequence of CAB1.4 gene

```
1  QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51  IDPENGDT EY APKFQ GKATF TTD TSSNTAY LQLSSLTSED TAVYYCNEGT
101 PTGPYYFDYW GQGTTVT VSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMKAQSV P GMAVAVIYQG KPHY YTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEV T DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGW EMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
```

Fig. 15H Amino acid sequence of CAB1.4 protein

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC(183)
H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCAG (273)
H3CDR (373) GGGCTCCCGACTGGGCCGTACTACTTTGACTAC(405)
L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC(582)
L2CDR (628) GATACATCCAACCTGGCTTCT(648)
L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG(771)

Fig. 15I Nucleotide sequences of CAB1.6 CDRs

```

1  CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCACCTGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGCTC
301 CCGACTGGGC CGTACTACTT TGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCAC TTC CAAACTC GTGATTTATG
551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTGATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCATATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

```

Fig. 15J Nucleotide sequence of CAB1.6 gene

```

1   CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51  AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCAGTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGCTC
301 CCGACTGGGC CGTACTACTT TGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAACCTC GTGATTTATG
551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGGCGGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GEGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTGATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCATATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CGCGTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

```

Fig. 15K Nucleotide sequence of CAB1.6i gene

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC(183)
H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG(273)
H3CDR (373) GGGCTCCCGCTCGGGGCCATTTACAACGACTAC(405)
L1CDR (553) AGTGCCAGCTCAGCTGTATATGCCATGCAC(582)
L2CDR (628) GATACATCCAACCTGGCTTCT(648)
L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG(771)

Fig. 15L Nucleotide sequences of CAB1.7 CDRs


```

1   CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGGCTC
51  AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCACCTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGGCTC
301 CCGCTCGGGG CCATTTACAA CGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAGCTG TATATGCCAT
501 GCACTGGTTC CAGCAGAAGC CAGGCAC TTC CAAACTC GTGATTTATG
551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTTCG GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTATCAA AACTGGCAGC
1151 CGCAGTGGA GCGCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAAGT GGTGATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

```

Fig. 15M Nucleotide sequence of CAB1.7 gene

```

1  CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCACTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGCTC
301 CCGCTCGGGG CCATTTACAA CGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAGCTG TATATGCCAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAATC GTGATTTATG
551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACCTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGGCGGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG AGGTACCGGA
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTCGG CTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCTCTTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GCGGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CGCGTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

```

Fig. 15N Nucleotide sequence of CAB1.7i gene

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC (183)
H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)
H3CDR (373) GGGACTCCGACTGGGCCGTACTACTTTGACTAC (405)
L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC (582)
L2CDR (628) AGCACATCCAACCTGGCTTCT (648)
L3CDR (745) CAGCAAAGATCTAGTTACCCACTCACG (771)

Fig. 150 Nucleotide sequences of CAB1 CDRs

```

1  CAGGTGAAAC TGCAGCAGTC TGGGGCAGAA CTTGTGAGGT CAGGGACCTC
51  AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCAC TGGTT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGACT
301 CCGACTGGGC CGTACTACTT TGA TACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCATGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAATC TGGATTTATA
551 GCACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGATCTAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGA GCGTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGT CATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTGAGACG AGTTTTGGTA
1601 ATGTAGCACT GCGCGCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

```

Fig. 15P Nucleotide sequence of CAB1 gene

H1CDR
(26) GFNIKDSYMH (35)
H2CDR (50) WIDPENGDT EYAPKFQ (65)
H3CDR (99) GLPLGAIYNDY (109)
L1CDR (159) SASSSVSYMH (168)
L2CDR (184) DTSNLAS (190)
L3CDR (223) QQRDSYPLT (231)

Fig. 15Q Amino acid sequences of SW149.5 CDRs

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC (183)
H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)
H3CDR (373) GGGCTCCCGCTCGGGGCCATTTACAACGACTAC (405)
L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC (582)
L2CDR (628) GATACATCCAACCTGGCTTCT (648)
L3CDR (745) CAGCAAAGAGATAGTTACCCACTCAG (771)

Fig. 15R Nucleotide sequences of SW149.5 CDRs

```

1  CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCACTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGCTC
301 CCGCTCGGGG CCATTTACAA CGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAACCTC GTGATTTATG
551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGA G CCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTGATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

```

Fig. 15S Nucleotide sequence of SW149.5 gene

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1  ACACCGGTGT CAGAAAAACA GCTGGCGGAG GTGGTCGCGA ATACGATTAC
51  CCCGCTGATG AAAGCCCAGT CTGTTCCAGG CATGGCGGTG GCCGTTATTT
101 ATCAGGGAAA ACCGCACTAT TACACATTTG GCAAGGCCGA TATCGCGGCG
151 AATAAACCCG TTACGCCTCA GACCCTGTTC GAGCTGGGTT CTATAAGTAA
201 AACCTTCACC GCGGTTTTAG GTGGGGATGC CATTGCTCGC GGTGAAATTT
251 CGCTGGACGA TCGGCTGACC AGATACTGGC CACAGCTGAC GGGCAAGCAG
301 TGGCAGGGTA TTCGTATGCT GGATCTCGCC ACCTACACCG CTGGCGGCCT
351 GCCGCTACAG GTACCGGATG AGGTCACGGA TAACGCCTCC CTGCTGCGCT
401 TTTATCAAAA CTGGCAGCCG CAGTGGAAGC CTGGCACAAAC GCGTCTTTAC
451 GCCAACGCCA GCATCGGTCT TTTTGGTGCG CTGGCGGTCA AACCTTCTGG
501 CATGCCCTAT GAGCAGGCCA TGACGACGCG GGTCCCTTAAG CCGCTCAAGC
551 TGGACCATAC CTGGATTAAC GTGCCGAAAG CGGAAGAGGC GCATTACGCC
601 TGGGGCTATC GTGACGGTAA AGCGGTGCGC GTTTCGCCGG GTATGCTGGA
651 TGCACAAGCC TATGGCGTGA AAACCAACGT GCAGGATATG GCGAACTGGG
701 TCATGGCAAA CATGGCGCCG GAGAACGTTG CTGATGCCTC ACTTAAGCAG
751 GGCATCGCGC TGGCGCAGTC GCGCTACTGG CGTATCGGGT CAATGTATCA
801 GGGTCTGGGC TGGGAGATGC TCAACTGGCC CGTGGAGGCC AACACGGTGG
851 TCGAGACGAG TTTTGGTAAT GTAGCACTGG CGCCGTTGCC CGTGGCAGAA
901 GTGAATCCAC CGGCTCCCCC GGTCAAAGCG TCCTGGGTCC ATAAAACGGG
951 CTCTACTGGC GGGTTTGGCA GCTACGTGGC CTTTATTCCT GAAAAGCAGA
1001 TCGGTATTGT GATGCTCGCG AATACAAGCT ATCCGAACCC GGCACGCGTT
1051 GAGGCGGCAT ACCATATCCT CGAGGCGCTA CAG

```

Fig. 15T Nucleotide sequence of BLA gene


```

1   CAGGTGAAAC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGGCTC
51  AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCACCTGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGACT
301 CCGACTGGGC CGTACTACTT TGA TACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GCGGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCATGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAATC GTGATTTATA
551 GCACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGATCTAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCTTAA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

```

Fig. 15U Nucleotide sequence of CAB1.1 gene

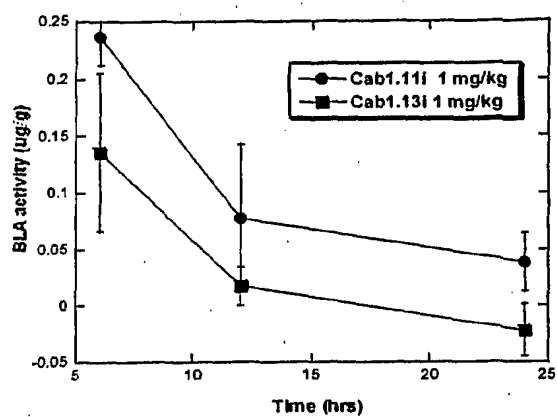


Figure 16

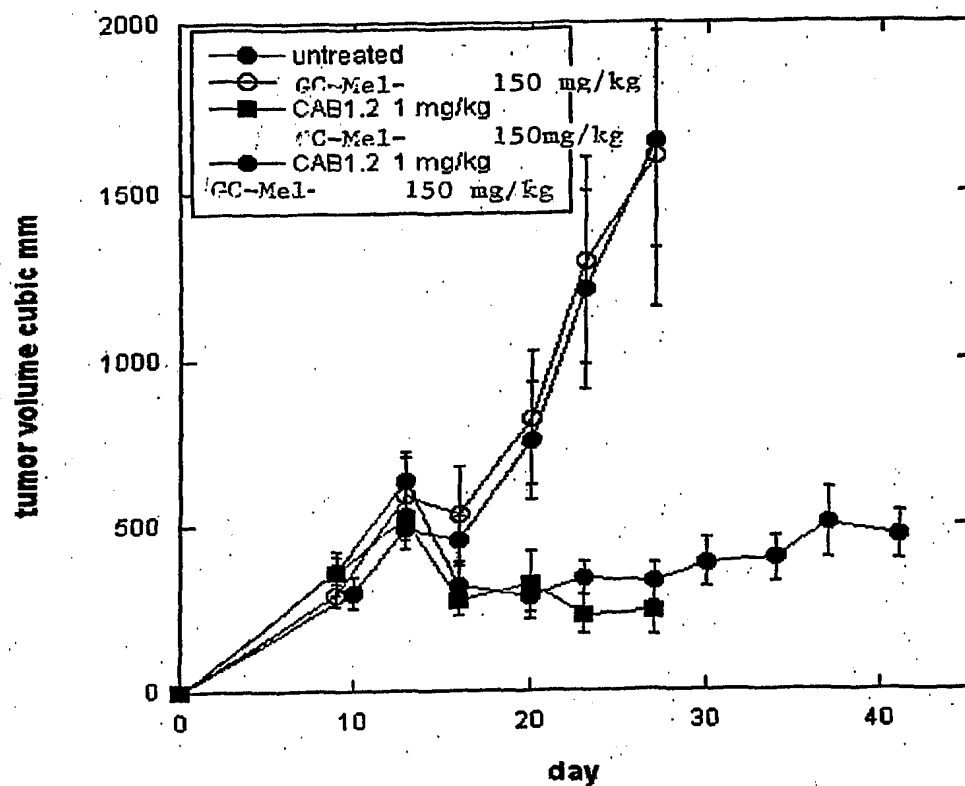


Figure 17

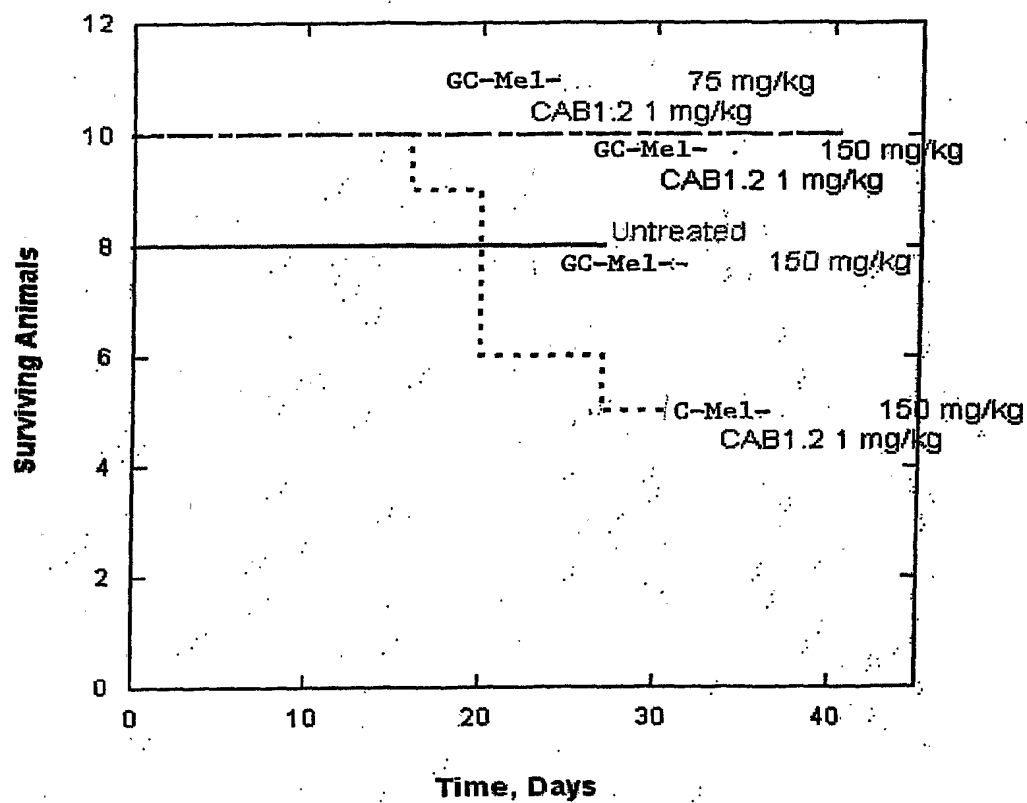


Figure 18

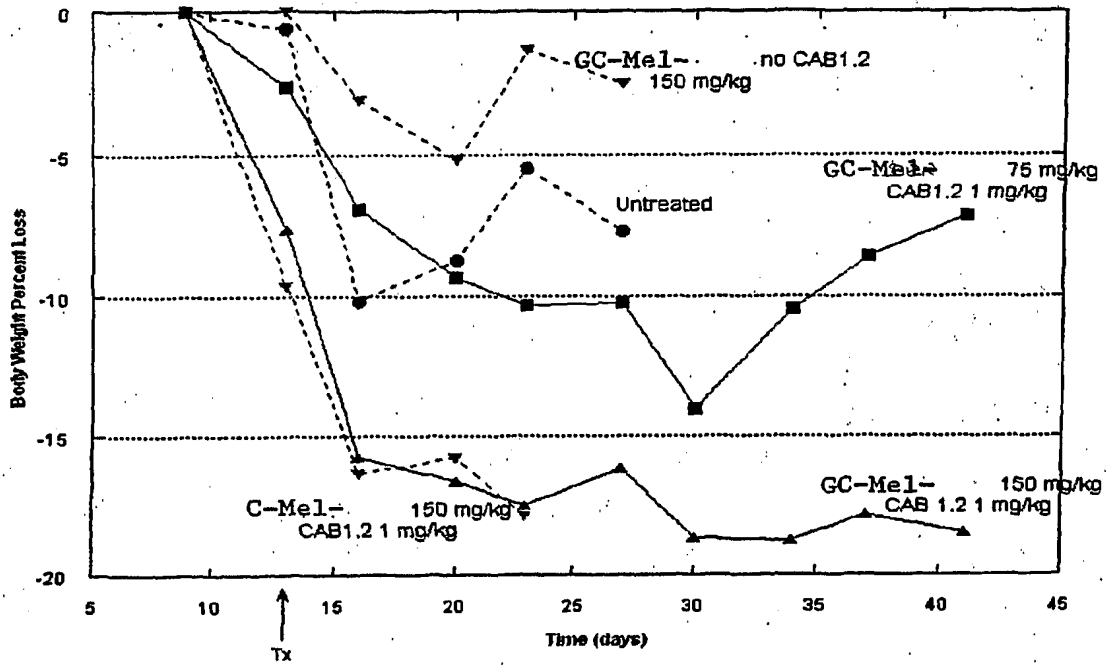


Figure 19

Animal weight effects

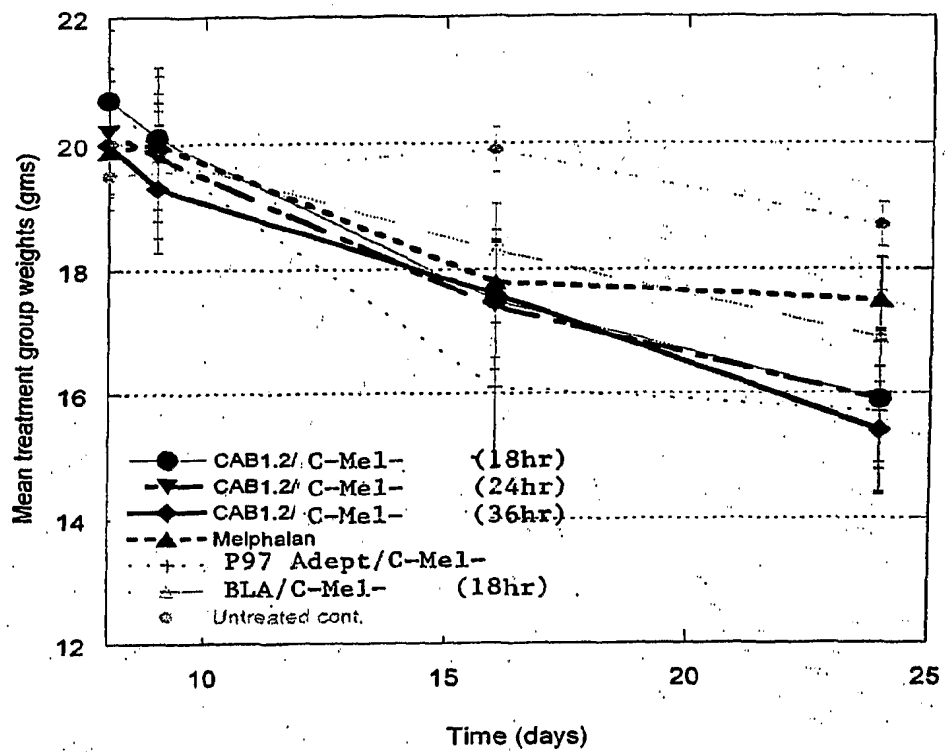


Figure 20

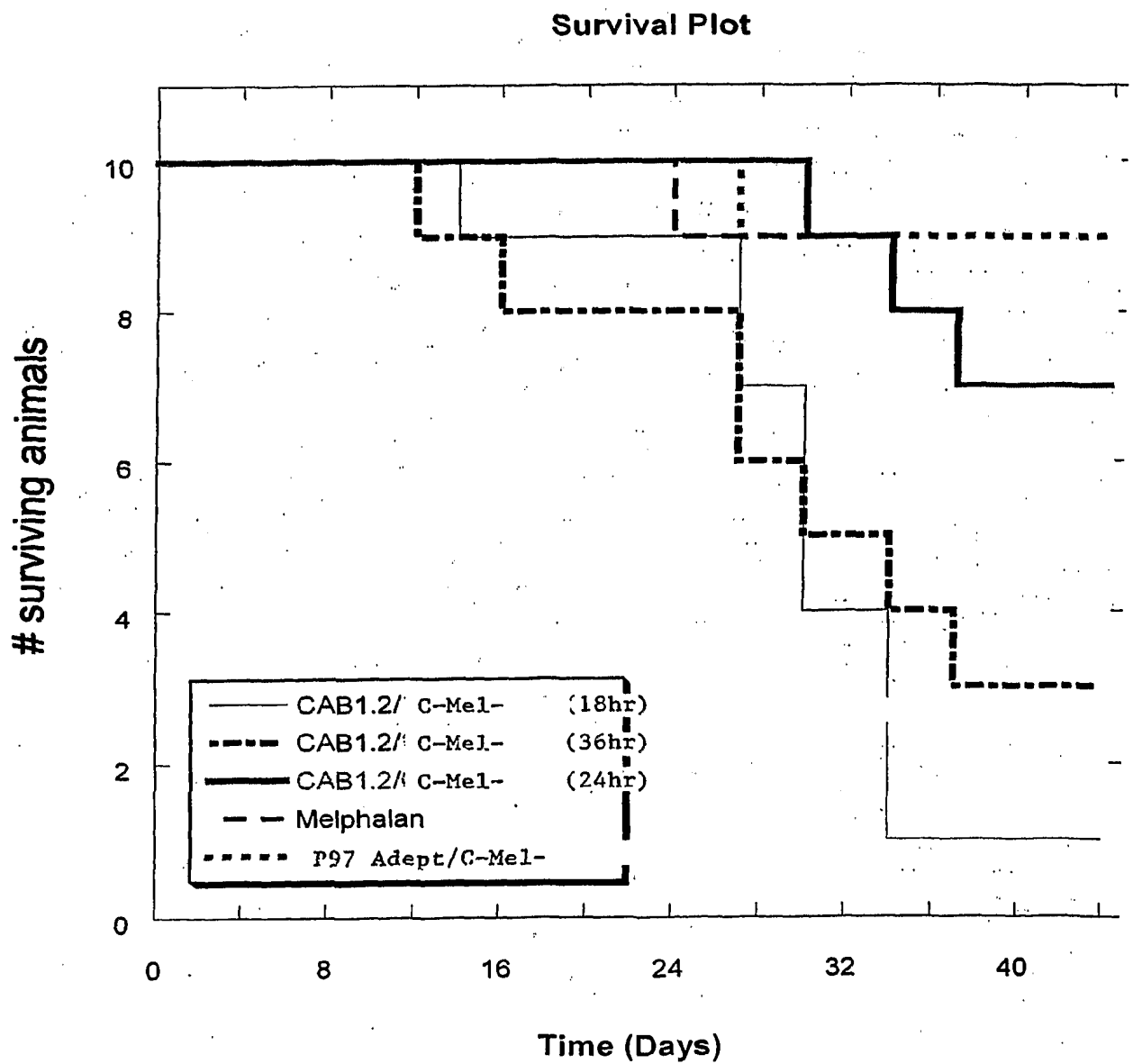
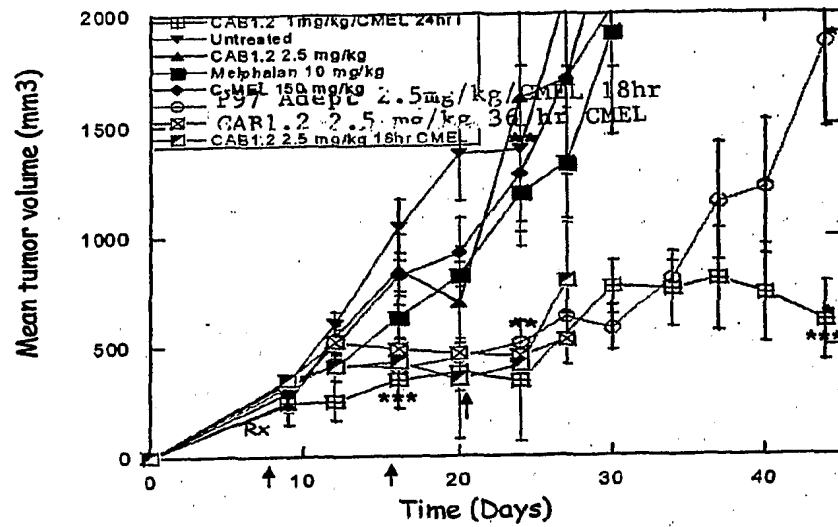


Figure 21

CAB1 Proof of Principle – Efficacy#

* $p < 0.05$ sgn17 vs CAB1.2(24h)

** $p < 0.05$ untreated vs CAB1.2(18,24,36h)

***GC observed in 2 animals: 1 Day 16; 1 Day 44

Figure 22

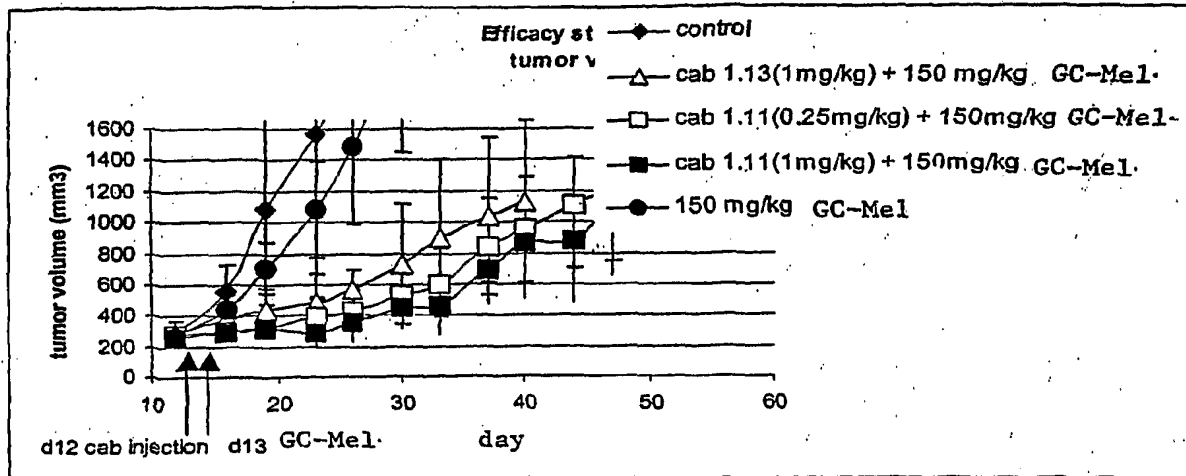


Figure 23

1 QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51 IDPENGDT EY APKFQ GKATF TTDTSNTAY LQLSSLTSED TAVYYCNEG T
101 PTGPYYFDYW GQGTTVT VSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYSTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRSSYPL TFGACTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMAAQSVPM GMAVAVIYQG KPHYTYFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGAYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ

Figure 24A

1 CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCAC TGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGACT
301 CCGACTGGGC CGTACTACTT TGA TACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GCGGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCAC TTC TCCCAA ACTC GTGATTTATA
551 GCACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGATCTAG TTACCCACTC ACSTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGGCGGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGCGT TTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGT CATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GCGGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CCGGTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

Figure 24B

1 QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51 IDPENGDTHEY APKFQ GKATF TTDTSNTAY LQLSSLTSED TAVYYCNEGL
101 PLGAIYNDYW GQGT TVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSAVYAMHWF QQKPGTSPKL VIYSTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMAAQSVPM GMAVAVIYQG KPHYTYTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGAYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ

Figure 24C

1 CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCAGTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGGCTC
301 CCGCTCGGGG CCATTTACAA CGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAGCTG TATATGCCAT
501 GCAGTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAATC GTGATTTATA
551 GCACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGGCGGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 GGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAAGT GGTGATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GCGGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CGCGTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

Figure 24 D

1	DIVLTQSPAS	LSVSLGQRAT	MSCRAGESVD	IFGVGFLHWY	QQKPGQPPKL
51	LIYRASNL	GIPVRFSGTG	SGTDFTLIID	PVEADADVATY	YCQQTNEDPY
101	TFGGGKLEI	KGGGSGGGG	SGGGSGGGG	SGGGSGGGG	SEVQLQQSGA
151	ELVEPGASVK	LSCTASGFNI	KDTYMHVVKQ	RPEQGLEWIG	RIDPANGNSK
201	YVPKFQKAT	ITADTSSNTA	YLQLTSLTSE	DTAVYYCAPF	GYVSDYAMA
251	YWGQGTSTV	SSTPVSEKQL	AEVVANTITP	LMAAQSVPGM	AVAVIYQGKP
301	HYTTFGKADI	AANKPVTPQT	LFELGSISK	FTGVLGGDAI	ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD	LATYTAGGLP	LQVPDEVTDN	ASLLRFYQNW
401	QPQWKPGTTR	LYANASIGLF	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451	INVPKAEAAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	DMANWVMANM
501	APENVADASL	KQGIALAQSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GVALAPLPV	AEVNPPAPPV	KASWVHKTGS	TGGFGAYVAF	IPEKQIGIVM
601	LANTSYPNPA	RVEAAYHILE	ALQ		

Figure 25A

1 GACATCGTCC TGACCCAGAG CCCGGCAAGC CTGTCTGTTT CCCTGGGCCA
51 GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG
101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAACTG
151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC
201 CGGTACTGGC TCTGGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG
251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC
301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG
351 TGGTGGTGGT AGCGGTGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG
401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG
451 GAGCTCGTTG AACC GGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG
501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC
551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA
601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC
651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG
701 TTTATTACTG CGCTCCGTTT GGCTACTATG TCAGCGATTA CGCAATGGCC
751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTGAGA
801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGGCGG
851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG
901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC
951 GCCTCAGACC CTGTTGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG
1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTTCGCT GGACGATGCG
1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTCTG
1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC
1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTTA TCAAAACTGG
1201 CAGCCGCACT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT
1251 CGGTCTTTTT GGTGCGCTGG CCGTCAAACC TTCTGGCATG CCCTATGAGC
1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG
1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA
1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG
1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG
1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC
1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG
1601 AGATGCTCAA CTGGCCCGTG GAGGCCAACA CGGTGGTCGA GACGAGTTTT
1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACCGGC
1701 TCCCCCGGTC AAAGCGTCCT GGGTCCATAA AACGGGCTCT ACTGGCGGGT
1751 TTGGCGCGTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG
1801 CTCGCGAATA CAAGCTATCC GAACCGGCA CGCGTTGAGG CGGCATACCA
1851 TATCCTCGAG GCGCTACAG

Figure 25B

Case ID	ASM	Sample ID	Sample Pathology
<u>CI0000000255</u>	DF5	FR00005C7B	Adenocarcinoma of lung
<u>CI00000005496</u>	FF5	FR5B337147	Adenocarcinoma of lung
<u>CI0000011577</u>	FF1	FR5B34059F	Adenocarcinoma of lung
<u>CI7000000241</u>	AF4	FR00033A78	Adenocarcinoma of lung
<u>CI0000007518</u>	AF5	FR0001FD15	Carcinoma of lung, squamous cell
<u>CI00000008475</u>	HF4	FR65EE0784	Adenocarcinoma of colon, metastatic
<u>CI0000015252</u>	FF2	FR5B342166	Adenocarcinoma of colon

Figure 26

26_A	26_B	26_C	26_D	26_E
26_F	26_G	26_H	26_I	26_J

FIGURE 26

FIG. 26 - A

Case Diagnosis	Tissue of Origin/Site of Finding	H/E	Anti-H
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>	Immunoger <u>4x</u>
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIB	Lung/Lung	<u>4X</u> <u>20X</u>	
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>	
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>	
Carcinoma of lung, squamous cell Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>	
Adenocarcinoma of colon, metastatic Grade: Not Reported Stage: IV	Colon/Liver	<u>4X</u> <u>20X</u>	Immune Fibr No <u>4x</u>
Adenocarcinoma of colon Grade: AJCC G3: Poorly differentiated Stage: IIIB	Cecum/Cecum	<u>4X</u> <u>20X</u>	

FIG. 26-3

Human Cytokeratin AE1/AE3	CAB/GCR3708 (0.2ug/ml)	CAB/GCR55*
ncity: Tumor(100%, Variable to 3+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 20x <u>SF00029758</u>	Immunogenicity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x <u>SF00029756</u>	Immunogenicity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x <u>SF000</u>
	Immunogenicity: Tumor(15%, Variable to 3+ Cyto) Intra-alveolar macrophages(Variable to 2+ Cyto) Mixed inflammatory cells(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF0002975B</u>	Immunogenicity: Tumor(15%, Variable to 3+ Cyto) Intra-alveolar macrophages(Variable to 2+ Cyto) Mixed inflammatory cells(Variable to 2+ Cyto) Specificity: High 4x <u>SF000</u>
	Immunogenicity: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x <u>SF0002977F</u>	Immunogenicity: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x <u>SF000</u>
	Immunogenicity: Tumor(75%, Variable to 3+ Cyto) Cellular Stroma(Variable to 2+ Cyto) Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF0002978B</u>	Immunogenicity: Tumor(75%, Variable to 3+ Cyto) Cellular Stroma(Variable to 2+ Cyto) Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to 2+ Cyto) Specificity: High 4x <u>SF000</u>
	Immunogenicity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x <u>SF0002975F</u>	Immunogenicity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x <u>SF000</u>
Immunogenicity: Tumor(98%, Variable to 3+ Cyto) Mem, Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Normal liver parenchyma(2+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 20x <u>SF0002976A*</u>	Immunogenicity: Tumor(95%, Variable to 3+ Cyto) Mem, Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Normal liver parenchyma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x <u>SF00029768</u> Normal liver parenchyma shows positive staining (1+)	Immunogenicity: Tumor(95%, Variable to 3+ Cyto) Mem, Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Normal liver parenchyma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x <u>SF000</u>
	Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Mem, Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF00029783</u>	Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Mem, Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High 4x <u>SF000</u>

FIG. 26-C

17 (0.2ug/ml)	CAB/GCR6798 (0.2ug/ml)	CAB/GCR8886 (0.196ug/ml)
<p>00%, Variable to 3+ Cyto) lls(Variable to 3+ Cyto) able to 2+ EC) ity: High <u>20x</u> <u>29757</u></p>	<p>Immunogenicity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029753</u></p>	<p>Immunogenicity: Tumor(100%, Variable Mixed inflammatory cells(Variable to Specificity: High <u>4x</u> <u>20x</u> <u>SF00029754</u></p>
<p>10%, Variable to 3+ Cyto) ges(Variable to 2+ Cyto) lls(Variable to 2+ Cyto) ity: High <u>20x</u> <u>2975C</u></p>	<p>Immunogenicity: Tumor(10%, Variable to 2+ Cyto) Intra-alveolar macrophages(Variable to 2+ Cyto) Mixed inflammatory cells(Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029759</u></p>	<p>Immunogenicity: Tumor(10%, Variable to Intra-alveolar macrophages(Variable to Mixed inflammatory cells(Variable to Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975A</u></p>
<p>nor(100%, 2+ Cyto) ma(1+ Cyto) ells(Variable to 1+ Cyto) ity: High <u>20x</u> <u>29780</u></p>	<p>Immunogenicity: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002977D</u></p>	<p>Immunogenicity: Tumor(100%, 2+ Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to Specificity: High <u>4x</u> <u>20x</u> <u>SF0002977E</u></p>
<p>15%, Variable to 3+ Cyto) ariable to 2+ Cyto) able to 2+ EC) ges(Variable to 2+ Cyto) ity: High <u>20x</u> <u>2978C</u></p>	<p>Immunogenicity: Tumor(75%, Variable to 3+ Cyto) Cellular Stroma(Variable to 2+ Cyto) Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029789</u></p>	<p>Immunogenicity: Tumor(75%, Variable to Cellular Stroma(Variable to 2+ C Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to Specificity: High <u>4x</u> <u>20x</u> <u>SF0002978A</u></p>
<p>nor(100%, 3+ Cyto) ma(1+ Cyto) able to 3+ EC) ity: High <u>20x</u> <u>29760</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975D</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975E</u></p>
<p>or(98%, Variable to 3+ e to 3+ Cyto) ariable to 1+ Cyto) nchyma(2+ Cyto) able to 3+ EC) ity: High <u>20x</u> <u>29769</u></p>	<p>Immunogenicity: Tumor(95%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Normal liver parenchyma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029765</u> Normal liver parenchyma shows positive staining (1+)</p>	<p>Immunogenicity: Tumor(95%, Variab Mem, Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ C Normal liver parenchyma(1+ Cy Necrosis(Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029766</u> Normal liver parenchyma shows positive s</p>
<p>or(85%, Variable to 3+ e to 3+ Cyto) ma(1+ Cyto) ariable to 2+ Cyto) ity: High <u>20x</u> <u>29784</u></p>	<p>Immunogenicity: Tumor(95%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029781</u></p>	<p>Immunogenicity: Tumor(95%, Variab Mem, Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ C Specificity: High <u>4x</u> <u>20x</u> <u>SF00029782</u></p>

FIG. 26-D

ml)	No Antibody control (Prediluted)
to 3+ Cyto) 1+ Cyto)	Immunogenicity: N/A Specificity: Unknown <u>SF00029755</u>
to 2+ Cyto) 2+ Cyto) 2+ Cyto)	
Cyto) 1+ Cyto)	
to 3+ Cyto) Cyto) 2+ Cyto)	
Cyto)	
ile to 3+ yto) to)	Immunogenicity: N/A Specificity: Unknown <u>SF00029767</u>
taining (1+)	
ile to 3+	
yto)	

FIG. 26-E

<u>CI0000017970</u>	HF1	FR65EE7B3D	Adenocarcinoma of colon
<u>CI0000010013</u>	AF2	FR00028F2E	Adenocarcinoma of pancreas, metastatic
<u>CI0000009651</u>	AF1	FR0002B111	Adenocarcinoma of pancreas, ductal
<u>CI0000008690</u>	CF4	FR00027B0E	Adenocarcinoma of pancreas, ductal
<u>CI0000007678</u>	AF3	FR0002575B	Adenocarcinoma of pancreas, ductal
<u>CI0000009736</u>	AF2	FR0002BAB4	Adenocarcinoma of pancreas, ductal

FIG. 26-F

Adenocarcinoma of colon Grade: AJCC G2: Moderately differentiated Stage: IIIC	Colon/Colon	<u>4X</u> <u>20X</u>	
Adenocarcinoma of pancreas, metastatic Grade: Not Reported Stage: IV	Pancreas/Omentum	<u>4X</u> <u>20X</u>	Immu Fibroa <u>4x</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u> <u>20X</u>	
Adenocarcinoma of pancreas, ductal Grade: AJCC G1: Well differentiated Stage: IIA	Pancreas/Pancreas	<u>4X</u> <u>20X</u>	
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: III	Pancreas/Pancreas	<u>4X</u> <u>20X</u>	
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u> <u>20X</u>	

FIG. 26-G

	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029787</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029787</u></p>
<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 1+ Cyto) Specificity: High</p> <p><u>20x</u> <u>SF0002977C</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002977A</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002977A</u></p>
	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029771</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029771</u></p>
	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002976D</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002976D</u></p>
	<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029763</u></p>	<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029763</u></p>
	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 2+ Cyto) Fibrotic stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029775</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 2+ Cyto) Fibrotic stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029775</u></p>

FIG. 26-H

<p>Immunogenicity: Tumor(100%, 3+ Cyto) Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x <u>SF00029788</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x <u>SF00029785</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x <u>SF00029786</u></p>
<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF0002977B</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF00029777</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF00029778</u></p>
<p>Immunogenicity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF00029772</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF00029770</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF0002976F</u></p>
<p>Immunogenicity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF0002976E</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF0002976B</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF0002976C</u></p>
<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High 4x 20x <u>SF00029764</u></p>	<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High 4x 20x <u>SF00029761</u></p>	<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High 4x 20x <u>SF00029762</u></p>
<p>Immunogenicity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Specificity: High 4x 20x <u>SF00029776</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Specificity: High 4x 20x <u>SF00029773</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 2+ Cyto) Fibrotic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF00029774</u></p>

FIG. 26-I

Cyto)	
Cyto) Cyto)	Immunogenicity: N/A Specificity: N/A <u>SF00029779</u>
Cyto) + Cyto)	
Cyto) yto)	
to 3+ Cyto) yto) Cyto)	
Cyto) Cyto) yto)	

FIG. 26-7

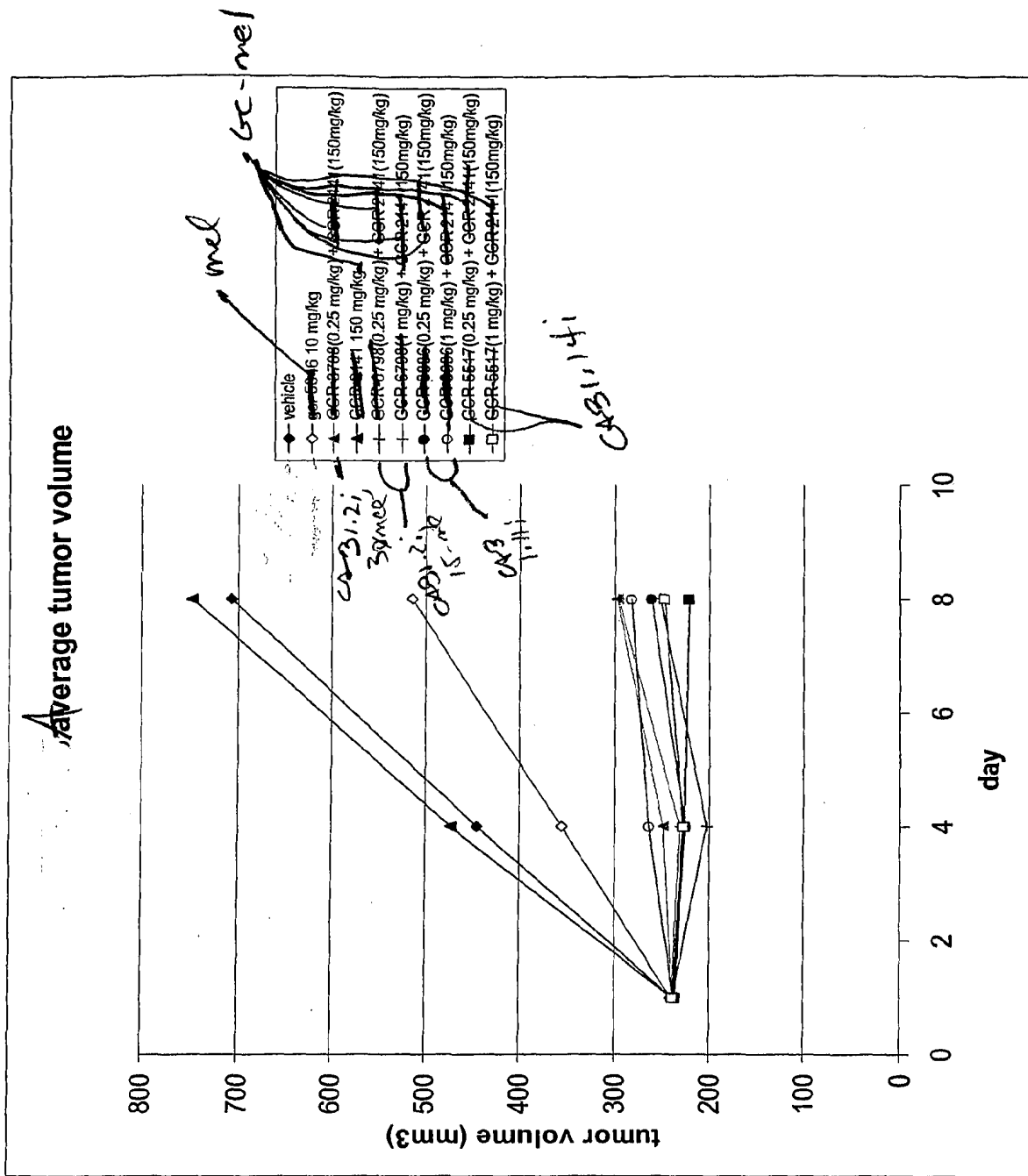


FIGURE 29A

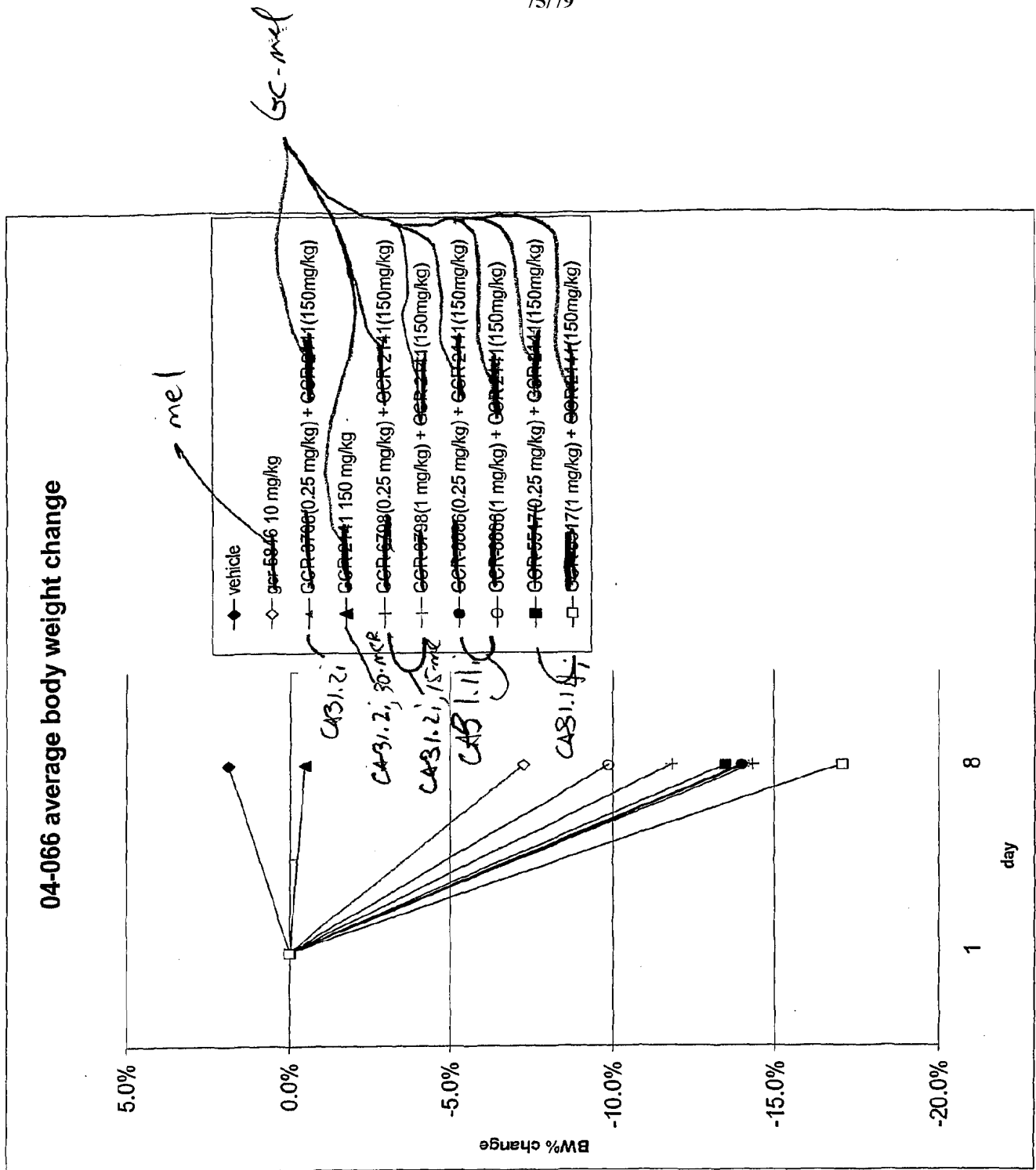


FIGURE 27B

Figure 28

GCR-Mel

Plasma GCR2141 concentration-time profiles (linear-linear scale)

Analyte=GCR2141

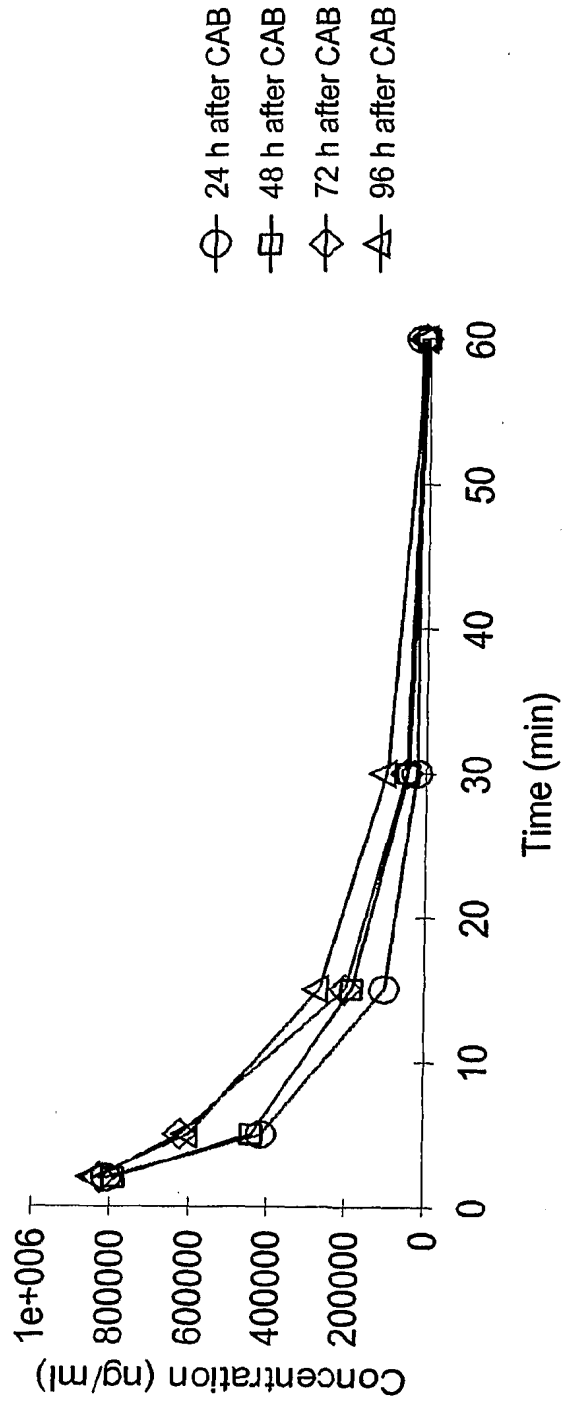
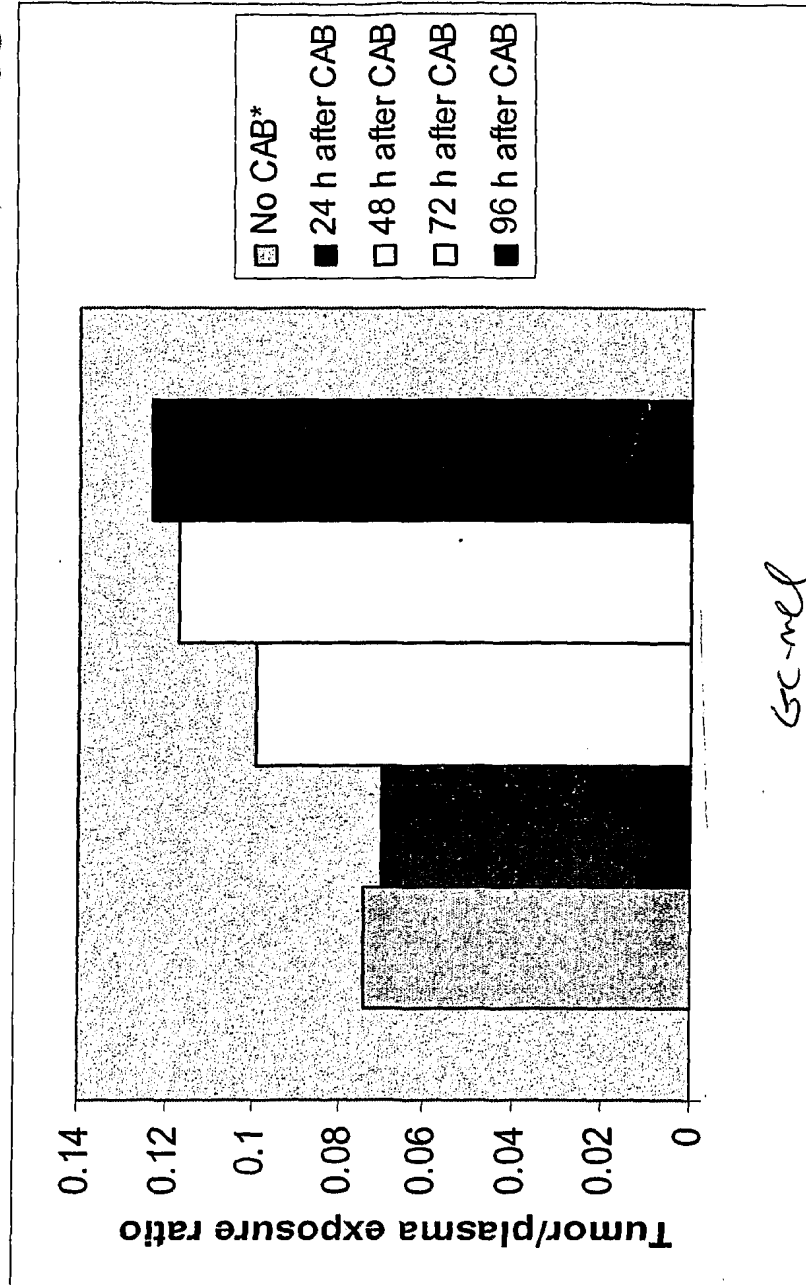


FIG 29A

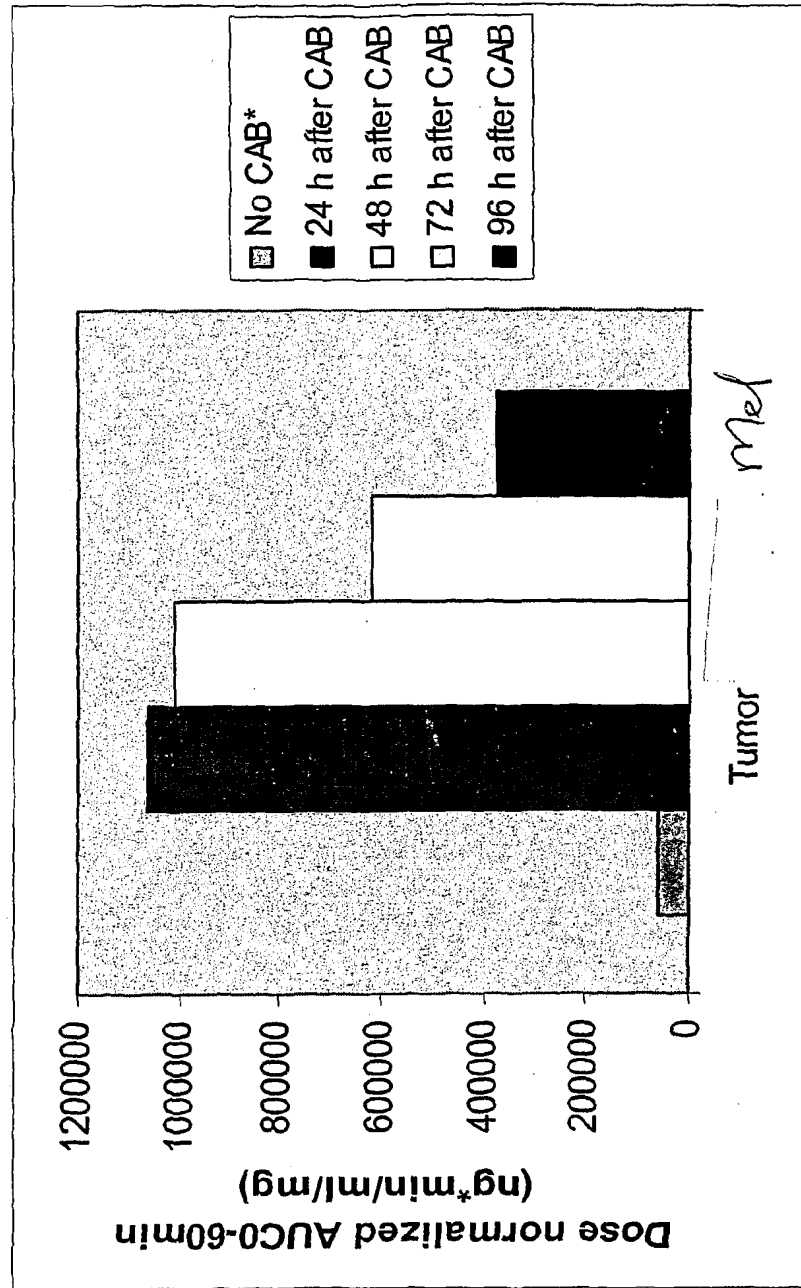
Tumor/Plasma
GC-mel
exposure
ratio



Data from study 04052, melphalan formulated in cyclodextrin

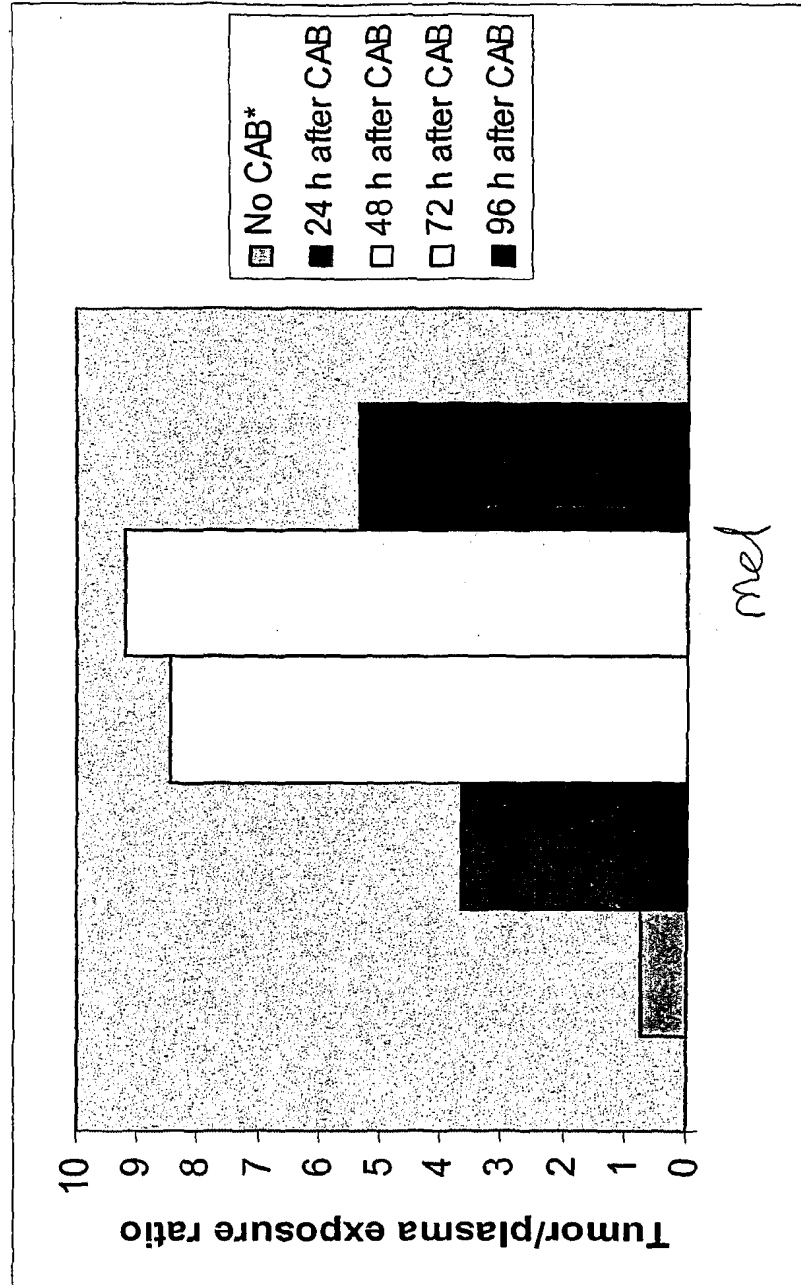
29B

mel
Tumor GCR ~~5846~~ exposure after ~~GCR 5846~~ *GSC-mel* administration



* Data from study 04052, melphalan formulated in cyclodextrin

Fig 29C - Tumor/plasma
mel exposure
ratio
After
GC-mel
Admin



* Data from study 04052, melphalan formulated in cyclodextrin